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AAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTGTTTTCATAAAGGATATTTATAAA
AAAAA

(SEQ ID NO: 1)

FIG. 1

Met	Asn	Gly	Glu	Ala	Ile	Cys	Ser	Ala	Leu	Pro	Thr	Ile	Pro	Tyr	His	Lys	Leu	Ala	Asp	20
Leu	Arg	Tyr	Leu	Ser	Arg	Gly	Ala	Ser	Gly	Thr	Val	Ser	Ser	Ala	Arg	His	Ala	Asp	Trp	40
Arg	Val	Gln	Val	Ala	Val	Lys	His	Leu	His	Ile	His	Thr	Pro	Leu	Leu	Asp	Ser	Glu	Arg	60
Lys	Asp	Val	Leu	Arg	Glu	Ala	Glu	Ile	Leu	His	Lys	Ala	Arg	Phe	Ser	Tyr	Ile	Leu	Pro	80
Ile	Leu	Gly	Ile	Cys	Asn	Glu	Pro	Glu	Phe	Leu	Gly	Ile	Val	Thr	Glu	Tyr	Met	Pro	Asn	100
Gly	Ser	Leu	Asn	Glu	Leu	Leu	His	Arg	Lys	Thr	Glu	Tyr	Pro	Asp	Val	Ala	Trp	Pro	Leu	120
Arg	Phe	Arg	Ile	Leu	His	Glu	Ile	Ala	Leu	Gly	Val	Asn	Tyr	Leu	His	Asn	Met	Thr	Pro	140
Pro	Leu	Leu	His	His	Asp	Leu	Lys	Thr	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Glu	Phe	His	Val	160
Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Trp	Arg	Met	Met	Ser	Leu	Ser	Gln	Ser	Arg	Ser	180
Ser	Lys	Ser	Ala	Pro	Glu	Gly	Gly	Thr	Ile	Ile	Tyr	Met	Pro	Pro	Glu	Asn	Tyr	Glu	Pro	200
Gly	Gln	Lys	Ser	Arg	Ala	Ser	Ile	Lys	His	Asp	Ile	Tyr	Ser	Tyr	Ala	Val	Ile	Thr	Trp	220
Glu	Val	Leu	Ser	Arg	Lys	Gln	Pro	Phe	Glu	Asp	Val	Thr	Asn	Pro	Leu	Gln	Ile	Met	Tyr	240
Ser	Val	Ser	Gln	Gly	His	Arg	Pro	Val	Ile	Asn	Glu	Gly	Ser	Leu	Pro	Tyr	Asp	Ile	Pro	260
His	Arg	Ala	Arg	Met	Ile	Ser	Leu	Ile	Glu	Ser	Gly	Trp	Ala	Gln	Asn	Pro	Asp	Glu	Arg	280
Pro	Ser	Phe	Leu	Lys	Cys	Leu	Ile	Glu	Leu	Glu	Pro	Val	Leu	Arg	Thr	Phe	Glu	Glu	Ile	300
Thr	Phe	Leu	Glu	Ala	Val	Ile	Gln	Leu	Lys	Lys	Thr	Lys	Leu	Gln	Ser	Val	Ser	Ser	Ala	320
Ile	His	Leu	Cys	Asp	Lys	Lys	Lys	Met	Glu	Leu	Ser	Leu	Asn	Ile	Pro	Val	Asn	His	Gly	340
Pro	Gln	Glu	Glu	Ser	Cys	Gly	Ser	Ser	Gln	Leu	His	Glu	Asn	Ser	Gly	Ser	Pro	Glu	Thr	360
Ser	Arg	Ser	Leu	Pro	Ala	Pro	Gln	Asp	Asn	Asp	Phe	Leu	Ser	Arg	Lys	Ala	Gln	Asp	Cys	380
Tyr	Phe	Met	Lys	Leu	His	His	Cys	Pro	Gly	Asn	His	Ser	Trp	Asp	Ser	Thr	Ile	Ser	Gly	400
Ser	Gln	Arg	Ala	Ala	Phe	Cys	Asp	His	Lys	Thr	Ile	Pro	Cys	Ser	Ser	Ala	Ile	Ile	Asn	420
Pro	Leu	Ser	Thr	Ala	Gly	Asn	Ser	Glu	Arg	Leu	Gln	Pro	Gly	Ile	Ala	Gln	Gln	Trp	Ile	440
Gln	Ser	Lys	Arg	Glu	Asp	Ile	Val	Asn	Gln	Met	Thr	Glu	Ala	Cys	Leu	Asn	Gln	Ser	Leu	460
Asp	Ala	Leu	Ser	Ser	Arg	Asp	Leu	Ile	Met	Lys	Glu	Asp	Tyr	Glu	Leu	Val	Ser	Thr	Lys	480
Pro	Thr	Arg	Thr	Ser	Lys	Val	Arg	Gln	Leu	Leu	Asp	Thr	Thr	Asp	Ile	Gln	Gly	Glu	Glu	500
Phe	Ala	Lys	Val	Ile	Val	Gln	Lys	Leu	Lys	Asp	Asn	Lys	Gln	Met	Gly	Leu	Gln	Pro	Tyr	520
Pro	Glu	Ile	Leu	Val	Val	Ser	Arg	Ser	Pro	Ser	Leu	Asn	Leu	Leu	Gln	Asn	Lys	Ser	Met	540

FIG. 2

(SEQ ID NO: 2)



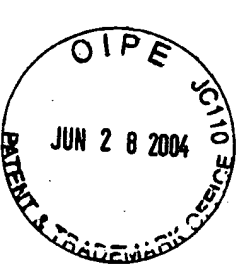
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CTGCTGAGAG GACACACGCA GCTGAAGATG AATTTGGGAA AAGTAGCCGC TTGCTACTTT
AACTATGGAA GAGCAGGGCC ACAGTGAGAT GGAAATAATC CCATCAGAGT CTCACCCCCA
CATTCAATTA CTGAAAAGCA ATCGGGAAC TCTGGTCACT CACATCCGCA ATACTCAGTG
TCTGGTGGAC AACTTGCTGA AGAATGACTA CTTCTCGGCC GAAGATGCGG AGATTGTGTG
TGCCTGCCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGGTAC AGAGCAAGGG
CGAGGAGGTG TCCGAGTTCT TCCTCTACTT GCTCCAGCAA CTCGCAGATG CCTACGTGGA
CCTCAGGCCT TGGCTGCTGG AGATCGGCTT CTCCCCTTCC CTGCTCACTC AGAGCAAAGT
CGTGGTCAAC ACTGACCCAG TGAGCAGGTA TACCCAGCAG CTGCGACACC ATCTGGGCCG
TGA CTCCAAG TTCGTGCTGT GCTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
CATGGACACC ATCATGGAGC TGGTTGGCTT CAGCAATGAG AGCCTGGGCA GCCTGAACAG
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CAGCTGCTTC AAGGAAAGTG ACAGGCTGTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
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CCTCTTCACC TTCGATGGCC TGGACGAGCT GCACTCGGAC TTGGACCTGA GCCGCGTGCC
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CTATGCCAGG AGGATGTTCC CCGAGCGGGC CCTGCAGGAC CGCCTGCTGA GCCAGCTGGA
GGCCAACCCC AACCTCTGCA GCCTGTGCTC TGTGCCCCCTC TTCTGCTGGA TCATCTTCCG
GTGCTTCCAG CACTTCCGTG CTGCCTTTGA AGGCTCACCA CAGCTGCCCCG ACTGCACGAT
GACCCTGACA GATGTCTTCC TCCTGGTCAC TGAGGTCCAT CTGAACAGGA TGCAGCCCAG
CAGCCTGGTG CAGCGGAACA CACGCAGCCC AGTGGAGACC CTCCACGCCG GCCGGGACAC
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CCAGGAGGAG GTGCAGGCCT CCGGGCTGCA GGAGAGAGAC ATGCAGCTGG GCTTCCTGCG
GGCTTTGCCG GAGCTGGGCC CCGGGGGTGA CCAGCAGTCC TATGAGTTTT TCCACCTCAC
CCTCCAGGCC TTCTTTACAG CCTTCTTCCT CGTGTGCTGAC GACAGGGTGG GCACTCAGGA
GCTGCTCAGG TTCTTCCAGG AGTGGATGCC CCCTGCGGGG GCAGCGACCA CGTCCTGCTA

FIG. 3A



TCCTCCCTTC CTCCCGTTCC AGTGCCTGCA GGGCAGTGGT CCGGCGCGGG AAGACCTCTT
CAAGAACAAG GATCACTTCC AGTTCACCAA CCTCTTCCTG TCGGGGCTGT TGTCCAAAGC
CAAACAGAAA CTCCTGCGGC ATCTGGTGCC CGCGGCAGCC CTGAGGAGAA AGCGCAAGGC
CCTGTGGGCA CACCTGTTTT CCAGCCTGCG GGGCTACCTG AAGAGCCTGC CCCGCGTTCA
GGTCGAAAGC TTCAACCAGG TGCAGGCCAT GCCCACGTTT ATCTGGATGC TCGCTGCAT
CTACGAGACA CAGAGCCAGA AGGTGGGGCA GCTGGCGGCC AGGGGCATCT GCGCCAACTA
CCTCAAGCTG ACCTACTGCA ACGCCTGCTC GGCCGACTGC AGCGCCCTCT CCTTCGTCCT
GCATCACTTC CCCAAGCGGC TGGCCCTAGA CCTAGACAAC AACAACTCTCA ACGACTACGG
CGTGCGGGAG CTGCAGCCCT GCTTCAGCCG CCTCACTGTT CTCAGACTCA GCGTAAACCA
GATCACTGAC GGTGGGGTAA AGGTGCTAAG CGAAGAGCTG ACCAAATACA AAATTGTGAC
CTATTTGGGT TTATACAACA ACCAGATCAC CGATGTCGGA GCCAGGTACG TCACCAAAT
CCTGGATGAA TGCAAAGGCC TCACGCATCT TAAACTGGGA AAAAACAAAA TAACAAGTA
AGGAGGGAAG TATCTCGCCC TGGCTGTGAA GAACAGCAAA TCAATCTCTG AGGTTGGGAT
GTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTC TCGGGAACCA
CCCCAGCTTG ACCACCCTGA GTCTTGCGTC CAACGGCATC TCCACAGAAG GAGGAAAGAG
CCTTGCGAGG GCCCTGCAGC AGAACACGTC TCTAGAAATA CTGTGGCTGA CCCAAAATGA
ACTCAACGAT GAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTTAAA
GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCCCAGC TGGCAGATGC
GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCCTAAAT GGAAACCTGA TAAAACCAGA
GGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTGT TTCTGAGAGG ATGCTTTTCT
GTTTATGGGG TTTTGGCCCT GGAGCCTCAG CAGCAAATGC CACTCTGGGC AGTCTTTTGT
GTCAGTGTCT TAAAGGGGCC TGCGCAGGCG GGAATATCAG GAGTCCACTG CCTYCATGAT
GCAAGCCAGC TTCCTGTGCA GAAGGTCTGG TCGGCAAACT CCCTAAGTAC CCGCTACAAT
TCTGCAGAAA AAGAATGTGT CTTGCGAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
GAAAAAAAAA ACGGACGCGT GG (SEQ ID NO: 7)

FIG. 3B



MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDFSAEDAEIVCACPTQP
DKVRKIIDLVSQSGEEVSEFFLYLLQOLADAYVDLRPWLLLEIGFSPSLLTQSKVVNTDPVSRYT
QQLRHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLSLSLACLLDHTTGILNEQG
ETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFRCRMFSCFKESDRICLQDILLFKHYCY
PERDPEEVFAFLLRFPHVAFVTFDGLDELHSDLDLSRVPDSSCPWEPAPHLVLLANLLSGKLLKG
ASKLLTARTGIEVPRQFLRKKVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCWIIIFRCFQHFRAAFEGSPQLPDCMTLTLDVFLLVTEVHLNRMQPSLQVRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELPGGDQQSYEFFHLL
QAFFTAFFLVLDLDRVGTQELLRFFQEWMPAGAAATTCYPPFLPFQCLQSGSPAREDLFKNKDH
QFTNLFCLGLLSKAKQKLLRHLVPAALRRKRKALWAHLFSSLRGYLKS LPRVQVESFNQVQAMP
TFIWMRLCIYETQSQKVGQLAARGICANYLKLTYCNACSDCSALS FVLHHPKRLALDLDNNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLGNKIITSEGGKYLA LAVKNSKSI SEVGMWGNQVGDGAKAF AEA LRNHPSLTTL
SLASNGISTEGGKSLARALQQNTSLEILWLTONELNDEVAESLAEMLKVNQTLKHLWLIQNQITA
KGTAQLADALQNTGITEICLNGNLIKPEEAKVYEDEKRIICF (SEQ ID NO: 8) **FIG. 4**



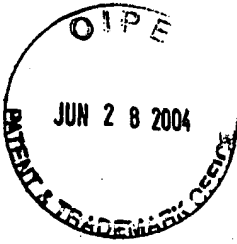
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AAGTCGTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGACACCATCTG
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ACCATCTTCATCCTGGGTGATGCTGGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCA
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AGCTGCCCCGACTGCACGATGACCCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCAT
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TGTTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTT
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CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTCATTGAAGAG
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GGTGAATAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAAGTGGGCCAGCAGAGCAT
GTTGGACACCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAGGGTGGGGGTGAT
ACTACTAGATCACTTGTCTCTTGCCAGCTCATTTGTTAATAAAATACTGAAAACACAA
AA
AAAAAAAAAAAA (SEQ ID NO: 25)

FIG. 5



HASDLLKNDYFSAEDAEIVCACPTQPDKVRKILDLVQSKGEEVSEFFLYLL
QQLADAYVDLRPWLLLEIGFSPSLLTQSKVVVNTDPVSRYTQQLRHHILGRDS
KFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSLACLDDHTTGILN
EQGETIFILGDAGVGKSMLLQRLQSLWATGRDLDAVKFFHFRCRMFSCFK
ESDRCLQDILLFKHYCYPERDPPEEVFAFLRRFPHVALLTFDGLDELHSDLD
LSRVPDSSCPWEPAHPLVLLANLLSGKLLKGASKLLTARTGIEVPRQFLRK
KVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSVPLFCWI
IFRCFQHFRAAFEGSPQLPDCMTLTVDVFLLVTEVHLNRMQPSLVQRNTR
SPVETLHAGRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFL
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FIG. 6



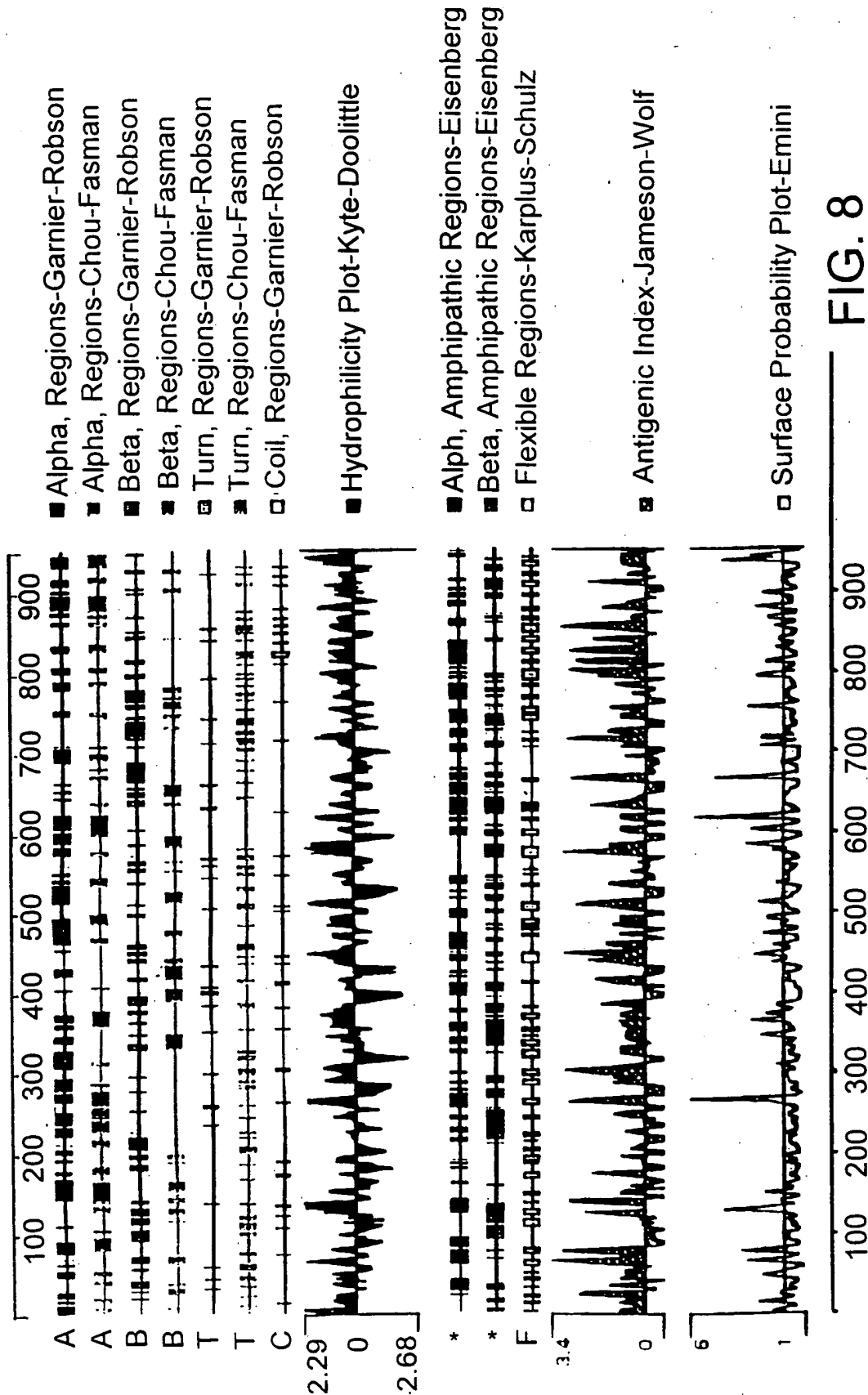
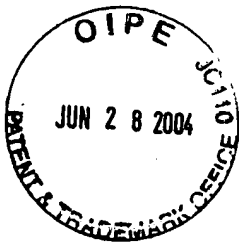
Applicant(s): John Bertin

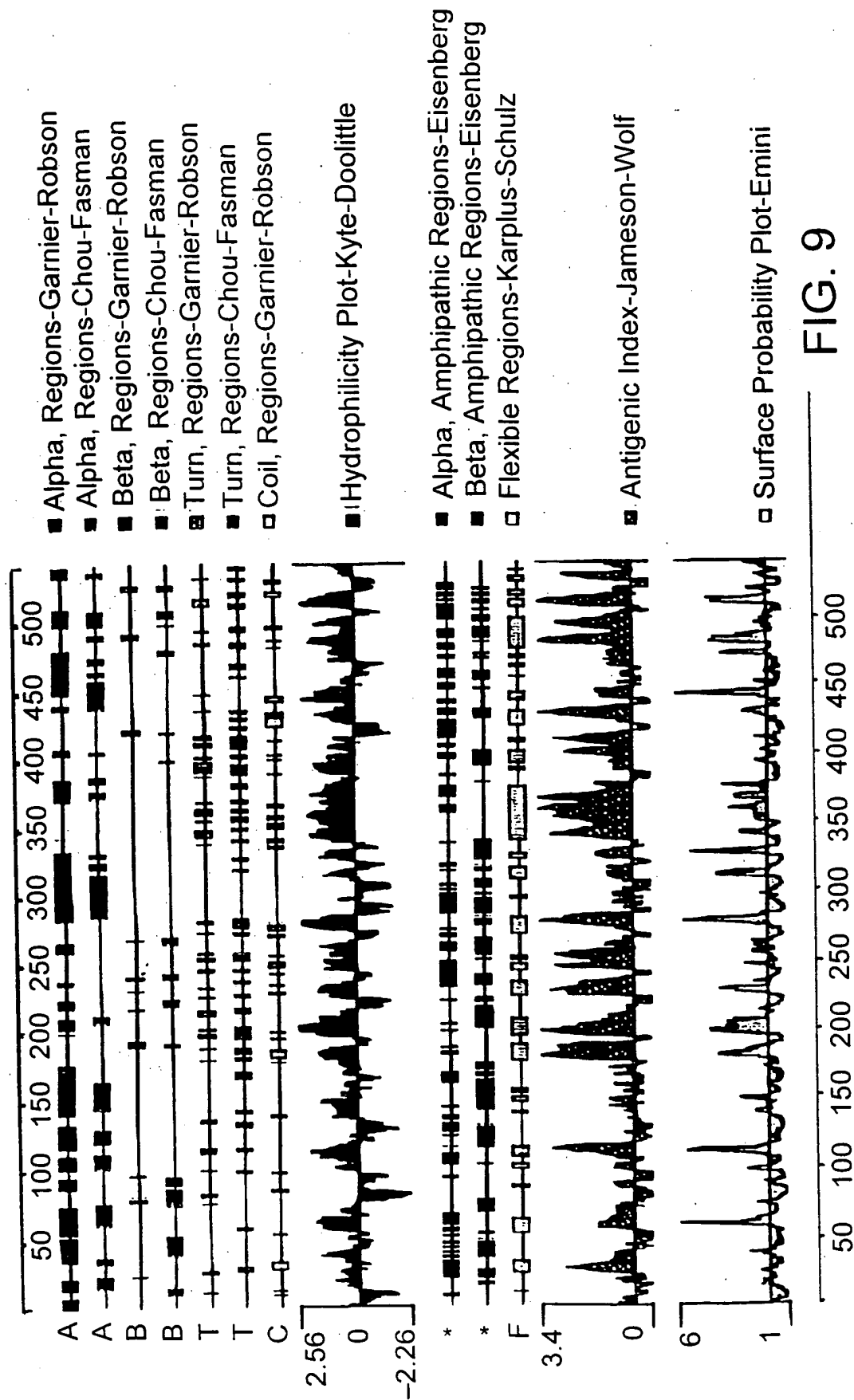
NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

SEQ. ID NO. 31/32/33/34

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11	L	-	Q	E	-	-	A	Q	S	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CARD3-CARD	
11	A	Q	E	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ARC-CARD		
11	M	A	S	D	N	D	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP1-CARD		
11	K	E	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP2-CARD		
36	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	L	V	Q	S	K	G	E	E	V	S	E	F	F	L	Y	L	CARD4-CARD	
39	I	M	K	E	D	Y	E	A	L	V	S	T	K	P	T	R	T	S	K	V	R	Q	L	L	D	T	T	D	I	Q	G	E	E	F	F	A	K	V	I	V	Q	K	CARD3-CARD
37	L	T	G	P	E	Y	E	A	L	D	A	L	P	D	A	E	R	R	V	R	Q	L	L	L	L	L	V	Q	G	K	G	E	A	A	C	Q	E	L	L	R	C	ARC-CARD	
36	I	N	K	Q	E	H	D	I	I	K	Q	K	T	Q	I	P	L	Q	A	R	E	L	I	D	T	I	W	V	K	G	N	A	A	A	A	N	I	F	K	N	C	CIAP1-CARD	
36	I	N	E	Q	E	H	D	I	I	K	Q	K	T	Q	I	P	L	Q	A	R	E	L	I	D	T	I	L	V	K	G	N	I	A	A	T	V	E	R	N	S	CIAP2-CARD		
76	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	-	-	L	L	E	I	G	F	S	P	S	L	L																CARD4-CARD
79	L	K	D	N	K	Q	-	-	M	G	L	Q	P	Y	P	E	I	L	V	S	R	S	P	S	L	L																	CARD3-CARD
77	A	Q	R	T	A	G	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ARC-CARD	
76	L	K	E	I	D	S	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP1-CARD	
76	L	Q	E	A	E	A	V	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP2-CARD	

FIG. 7

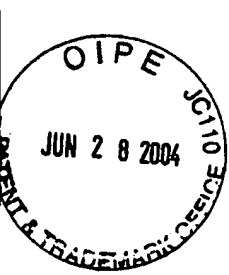






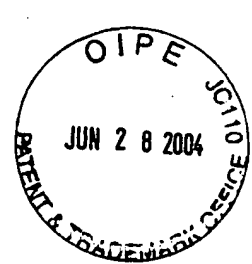
CCCGCGTCCGCGTCCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCT
GCGAAGTCTGTNAACCTGGTGGCCAAGTGATTGTAAGTCAGGAGACTTTCCTTCGGTTTC
TGCCTTTGATGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAACATCTGGGAAGAC
AAGTTGCTGTTTTTATGGGAATCGCAGGCTTGGAAGAGACAGAAGCAATTCCAGAAATAA
ATTGGAAATTGAAGATTTAAACAATGTTGTTTTTAAATATTCTAACTTCAAAGAATGATG
CCAGAAACTTAAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCTGGAGGGCGCGGCCTGAAT
CCTGATTGCCCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGC
CGCTTGCTACTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAG
AGTCTCACCCCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCC
GCAATACTCAGTGTCTGGTGGACAACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATG
CGGAGATTGTGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGG
TACAGAGCAAGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCGCAG
ATGCCTACGTGGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCA
CTCAGAGCAAAGTCGTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGAC
ACCATCTGGGCCGTGACTCCAAGTTCGTGCTGTGCTATGCCCAGAAGGAGGAGCTGCTGC
TGGAGGAGATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGG
GCAGCCTGAACAGCCTGGCCTGCCTCCTGGACCACACCACCGGCATCCTCAATGAGCAGG
CTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTCAAGCACTACTGCTA
CCCAGAGCGGGACCCCGAGGAGGTGTTTGCCTTCCTGCTGCGCTTCCCCACGTGGCCCT
CTTACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTGAGCCTGAGCCGCGTGCCTGA
CAGCTCCTGCCCCCTGGGAGCCTGCCCACCCCTGGTCTTGCTGGCCAACCTGCTCAGTGG
GAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCGCACAGGCATCGAGGTCCCGCG
CCAGTTCCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCCCAGCCACCTGCGCGCCTA
TGCCAGGAGGATGTTCCCCGAGCGGGCCCTGCAGGACCGCCTGCTGAGCCAGCTGGAGGC
CAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCCCTCTTCTGCTGGATCATCTTCCGGTG
CTTCCAGCACTTCCGTGCTGCCTTTGAAGGCTCACCACAGCTGCCCGACTGCACGATGAC
CCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCATCTGAACAGGATGCAGCCCAGCAG
CCTGGTGCAGCGGAACACACGCAGCCAGTGGAGACCCTCCACGCCGGCCGGGACACTCT
GTGCTCGCTGGGGCAGGTGGCCACCGGGGCATGGAGAAGAGCCTCTTTGTCTTACCCA
GGAGGAGGTGCAGGCCTCCGGGCTGCAGGAGAGAGACATGCAGCTGGGCTTCTGCGGGC
TTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCAGTCCTATGAGTTTTTCCACCTCACCT

FIG. 10A



CCAGGCCTTCTTTACAGCCTTCTTCCTCGTGCTGGACGACAGGGTGGGCACTCAGGAGCT
GCTCAGGTTCTTCCAGGAGTGGATGCCCCCTGCGGGGGCAGCGACCACGTCCTGCTATCC
TCCCTTCTTCCCGTTCCAGTGCCTGCAGGGCAGTGGTCCGGCGCGGGAAGACCTCTTCAA
GAACAAGGATCACTTCCAGTTCACCAACCTCTTCCTGTGCGGGCTGTTGKCCAAAGCCAA
ACAGAACTCCTGCGGCATCTGGTGCCCCGCGGCAGCCCTGAGGAGAAAGCGCAAGGCCCT
GTGGGCACACCTGTTTTCCAGCCTGCGGGGCTACCTGAAGAGCCTGCCCCGCGTTCAGGT
CGAAAGCTTCAACCAGGTGCAGGCCATGCCCACGTTTCATCTGGATGCTGCGCTGCATCTA
CGAGACACAGAGCCAGAAGGTGGGGCAGCTGGCGGCCAGGGGCATCTGCGCCAACTACCT
CAAGCTGACCTACTGCAACGCCTGCTCGGCCGACTGCAGCGCCCTCTCCTTCGTCCTGCA
TCACTTCCCCAAGCGGCTGGCCCTAGACCTAGACAACAACAATCTCAACGACTACGGCGT
GCGGGAGCTGCAGCCCTGCTTCAGCCGCCTCACTGTTCTCAGACTCAGCGTAAACCAGAT
CACTGACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTGACCTA
TTTGGGTTTATACAACAACCAGATCACCGATGTCTGGAGCCAGGTACGTCACCAAAATCCT
GGATGAATGCAAAGGCCTCACGCATCTTAACTGGGAAAAAACAAAATAACAAGTGAAGG
AGGGAAGTATCTCGCCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTG
GGGCAATCAAGTTGGGGATGAAGGAGCAAAAGCCTTCGCAGAGGCTCTGCGGAACCACCC
CAGCTTGACCACCCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCT
TGCGAGGGCCCTGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACT
CAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCA
TTTATGGCTTATCCAGAATCASATCACAGCTWARGGGACTGCCCAGCTGGCAGATGCGTT
ACAGAGCAACACTGGCATAACAGAGATTTGCCTAAATGGAAACCTGATAAAACCAGAGGA
GGCCAAAGTCTATGAAGATGAGAAGCGGATTATCTGTTTCTGAGAGGATGCTTTCCTGTT
CATGGGGTTTTTGGCCCTGGAGCCTCAGCAGCAAATGCCACTYTGGGCAGTCTTTTGTGTC
AGTGTCTTAAAGGGGCCTGCGCAGGCGGGACTATCAGGAGTCCACTGCCTCCATGATGCA
AGCCAGCTTCCTGTGCAGAAGGTCTGGTCCGCAAACCTCCCTAAGTACCCGCTACAATTCT
GCAGAAAAAGAATGTGTCTTGCGAGCTGTTGTAGTTACAGTAAATACACTGTGAAGAGAC
TTTATTGCCTATTATAATTATTTTTATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACA
GAGGAGGCCAGCCTCACCTCATTCCAACACCTGCCATAGGGACCAACGGGAGCGAGTTGG
TCACCGCTCTTTTCATTGAAGAGTTGAGGATGTGGCACAAAGTTGGTGCCAAGCTTCTTG
AATAAACGTGTTTGATGGATTAGTATTATACCTGAAATATTTTCTTCTCCTTCTCAGCACT
TTCCCATGTATTGATACTGGTCCCCTTCACAGCTGGAGACACCGGAGTATGTGCAGTGT
GGGATTTGACTCCTCCAAGGTTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGG

FIG. 10B



GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCTCCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAACTGG
GCCAGCAGAGCATGTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGCCAGCTCATTTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO: 38)

FIG. 10C

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPDKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLLEIGFSPSLLTQSKVV
VNTDPVSRYTQQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSL
ACLLDHTTGILNEQAASRKVTGCVCRTCSSSTTATQSGTPRRCLPSCCASPTWPSSPSMA
WTSCIRTW (SEQ ID NO: 39)

FIG. 11



CACGCGTCCGCGCTACTGCGGGAGCAGCGTCCTCCCGGGCCACGGCGCTTCCCGGCCCCG
GCGTCCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCTGCGAAGTCT
GTAAACCTGGTGGCCAAGTGATTGTAAGTCAGGAGACTTTCTTTCGGTTTCTGCCTTTGA
TGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAACATCTGGGAAGACAAGTTGCTG
TTTTTATGGGAATCGCAGGCTTGGAAGAGACAGAAGCAATTCCAGAAATAAATTGGAAAT
TGAAGATTTAAACAATGTTGTTTTTAAATATTCTAAGTCAAGAAATGATGCCAGAACT
TAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCTGGAGGGCGCGGCCTGAATCCTGATTGC
CCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
CTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
CCCACATTCAATTACTGAAAAGCAATCGGGAAGTCTGGTCACTCACATCCGCAATACTC
AGTGTCTGGTGGACAACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
TGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCGCAAATTTCTGGACCTGGTACAGAGCA
AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCGCAGATGCCTACG
TGGACCTCAGGCCTTGCTGCTGGAGATCGGCTTCTCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCAGT
GCAAGCAGGGCCCTGGGGGGTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
AGCAGGCCCAGGTGCTATTTTGATTTTAGAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
CAGCCCAGGTGGCTGCGATTGAACTGCCCCACACCTCGATGGTCTGGTTTATAGAGGGGCC
TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTCTATTCTGACATAT
GTAGACATTTTAATGGTTGCACAAATTCAAGGTTGTATTTTTTTTTCTTTAAAAAATCT
TTAGCTGGACATGGTAGCACACACCTGTAGTTCCAGCTACTCAGGAGGCTGAGGCAAGAG
GACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCCTACACTCCA
CAGCCTGGGTTTTAGAGTGAGACCCTGTCTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAANGGGCGG (SEQ ID NO: 40)

FIG. 12

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPDKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLLEIGFSPSLLTQSKVV
VNTDPGRSQPQQDRRHQCKQGPGGFGNGWASPECHLRKQAQVLF

(SEQ ID NO: 41)

FIG. 13



	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	Majority		
											10										20																		30				40
1	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	CARD4-Y CLONE		
1	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	CARD4-Z CLONE		
1	M	E	E	Q	G	H	S	E	M	E	I	I	P	S	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	CARD4L		
	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	Majority		
											50										60																	70				80	
41	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	CARD4-Y CLONE		
41	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	CARD4-Z CLONE		
41	V	D	N	L	L	K	N	D	Y	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	CARD4L		
	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	Majority		
											90										100																	110				120	
81	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	CARD4-Y CLONE		
81	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	CARD4-Z CLONE		
81	E	V	S	E	F	F	L	Y	L	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	L	L	E	I	G	F	S	P	S	L	L	T	Q	S	K	V	V	CARD4L		
	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	Majority		
											130										140																	150				160	
121	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	CARD4-Y CLONE		
121	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	CARD4-Z CLONE		
121	V	N	T	D	P	V	S	R	Y	T	Q	Q	L	R	H	H	L	G	R	D	S	K	F	V	L	C	Y	A	Q	K	E	E	L	L	L	E	E	I	Y	M	CARD4L		

FIG. 14A



	- - - - -	T X X T X X X P R - - - - -	- - - - -	- - - - -	Majority
	330		340	350	360
212	- - - - -	T T A T Q S G T P R - - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
321	K L L K G A S K L L T A R T G I E V P R Q F L R K K V L L R G F S P S H L R A Y				CARD4L
	- - - - -	- - - - -	- - - - -	- - - - -	R C Majority
	370		380	390	400
222	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
361	A R R M F P E R A L Q D R L L S Q L E A N P N L C S L C S V P L F C W I I F R C				CARD4L
	- - - - -	- - - - -	- - - - -	- - - - -	Majority
	410		420	430	440
224	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
401	F Q H F R A A F E G S P Q L P D C T M T L T D V F L L V T E V H L N R M Q P S S				CARD4L
	- - - - -	- - - - -	- - - - -	- - - - -	Majority
	450		460	470	480
228	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Y CLONE
141	- - - - -	- - - - -	- - - - -	- - - - -	CARD4-Z CLONE
441	L V Q R N T R S P V E T L H A G R D T L C S L G Q V A H R G M E K S L F V F T Q				CARD4L

FIG. 14C



	- - - - - X X P X X X W - - - - -	Majority
	650 660 670 680	
235	- - - - - S S P S M A W - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - - - - - - -	CARD4-Z CLONE
641	E S F N Q V Q A M P T F I W M L R C I Y E T Q S Q K V G Q L A A R G I C A N Y L	CARD4L
	- - - - - X X C X X X - - - - -	Majority
	690 700 710 720	
242	- - - - - T S C T R T - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - - - - - - -	CARD4-Z CLONE
681	E L T Y C N A C S A D C S A L S F V L H H F P K R L A L D L D N N N L N D Y G V	CARD4L
	- - - - - - - - - - - - - - - - -	Majority
	730 740 750 760	
248	- - - - - - - - - - - - - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - - - - - - -	CARD4-Z CLONE
721	R E L Q P C F S R L T V L R L S V N Q I T D G G V K V L S E E L T K Y K I V T Y	CARD4L
	- - - - - - - - - - - E C X - - - - -	Majority
	770 780 790 800	
248	- - - - - - - - - - - - - - - - -	CARD4-Y CLONE
153	- - - - - - - - - - - E C H - - - - -	CARD4-Z CLONE
761	L G L Y N N Q I T D V G A R Y V T K I L D E C K G L T H L S L Y N N Q I T D V G	CARD4L

FIG. 14E



	810	820	830	840	Majority
	---	---	---	W X X X X X X X X	
248	---	---	---	---	CARD4-Y CLONE
156	---	---	---	W T	CARD4-Z CLONE
801	A R L G K N K I T S E G G K Y L A L A V K N S K S I S E V G M W G N Q V G D E G				CARD4L
	850	860	870	880	Majority
	---	---	---	---	
249	---	---	---	---	CARD4-Y CLONE
156	---	---	---	---	CARD4-Z CLONE
841	A K A F A E A L R N H P S L T T L S L A S N G I S T E G G K S L A R A L Q Q N T				CARD4L
	890	900	910	920	Majority
	---	---	---	---	
249	---	---	---	---	CARD4-Y CLONE
161	---	---	---	---	CARD4-Z CLONE
881	S L E I L W L T Q N E L N D E V A E S L A E M L K V N Q T L K H L W L I Q N Q I				CARD4L
	930	940	950	960	Majority
	---	---	---	---	
249	---	---	---	---	CARD4-Y CLONE
164	---	---	---	---	CARD4-Z CLONE
921	T A K G T A Q L A D A L Q S N T G I T E I C L N G N L I K P E E A K V Y E D E K				CARD4L

FIG. 14F



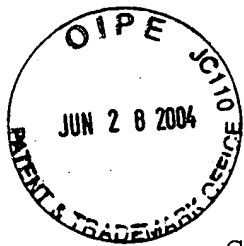
Applicant(s): John Bertin

NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

Majority	
	CARD4-Y CLONE
	CARD4-Z CLONE
	CARD4L
X X X X F	
249	
164	- - - F
961	R I I C F

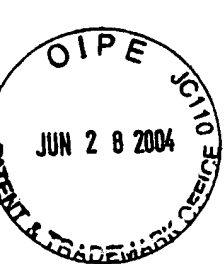
Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 14G



CCACGCGTCCGCGGACCGCGAGCGGTAGCGCCCTCCCTCCCAGCTGTTGTCCCGCCCGAT
CCGCGACCCTAGTCCCCGGATCCCCTTGCTGAGAGTCACCGTACTCCAGGGCCAACTGAG
CCAAAGTCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
TCCTGATTTGTCTGCCCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
TGGGTTGTCACTCCACATTAAACTGCTGAAGATCAACAGGGAACATCTGGTCACCAACA
TTCGGAACACTCAGTGTCTGGTGGACAACTTGTCTGGAGAATGGCTACTTCTCAGCCGAAG
ATGCAGAGATTGTGTGTGCCTGTCCCACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCCTCTACGTGCTGCAGCAGCTGG
AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCCCTTCCCAGC
TCATTCCGACCAAACTATCGTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
GACACCAACTGGGCGCGACTCCAAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTGC
TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACC
TGGGCAGCCTAGGAGGCCTGGATTGCCTGCTGGACCACAGTACGGGCGTCTCAACGAGC
ATGGCGAGACTGTCTTCGTGTTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGA
GGTTGCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
TCCGCTGCCGCATGTTTCACTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
TCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTGC
GCTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
ACCTGAGCCGCGTGCCGGATAGCTGCTGCCCTGGGAGCCGGCTCACCTCTGGTCTGCTGC
TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCTCGCA
CAGGCGTGAGGTTCCCCCGCCAGCTCCTGCGCAAAAAGGTGCTGCTCCGGGGCTTCTCCC
CAAGTCACCTGCGCGCCTATGCCCCGCCGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
TGCTGCAGCAGCTGGATGCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
AGTTGCCGGACTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
TGAACAGGCCGCGAGCCAGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCC
TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACA
AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCGAAGCTGCAGGAAGGAGATC
TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACG
AATTTTCCACCTTACGCTCCAGGCCTTCTTCACCGCCTTCTTCCTGGTAGCAGATGACA
AAGTGAGCACCCGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCCTGGAGAGGCAA

FIG. 15A



CAAGCTCGTCCTGCCATTCTTCCTTCTTCTCCTTCCAGTGCCTGGGCGGCAGAAGCCGGT
TGGGCCCTGATCCTTTTCAGGAACAAAGATCACTTCCAGTTCACCAACCTCTTCGTGTGCG
GGCTACTGGCCAAAGCCCGACAGAACTCCTTCGGCAGCTGGTGCCCAAGGCTATCCTGA
GGAGGAAGCGCAAGGCCCTGTGGGCTCACCTGTTTGCTAGCCTGCGCTCCTACTTGAAGA
GCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCACATTCCTGT
GGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCCGCCAGGG
GCATCAGTGCGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGACTGCAGCG
CCCTGTCTCTTCGTCTGCATCACTTCCACAGGCAGCTGGCCCTAGACCTGGACAACAACA
ACCTCAATGACTATGGCGTGCAGGAGCTGCAGCCTTGCTTTAGCCGTCTCACGGTTATCA
GACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAGGTGCTATGTGAGGAACTGACCA
AGTATAAGATCGTGACGTTCTTGGGTTTATACAACAACCAGATAACTGATATCGGAGCCA
GGTATGTGGCCCAAATCCTGGATGAATGCAGAGGCCTCAAGCACCTTAAACTAGGGAAAA
ACAGAATAACAAGTGAGGGCGGGAAGTGTGTGGCTTTGGCTGTGAAGAACAGCACCTCCA
TCGTTGATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAG
AGGCATTGAAGGACCACCCAGCCTGACCACTCTCAGTCTTGCAATTCAATGGCATCTCTC
CGGAGGGAGGGAAGAGCCTTGCGCAGGCCCTGAAGCAGAACACCACACTGACAGTAATCT
GGCTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAG
TGAACCAGACGCTACGGCATTTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACAG
CGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGAA
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GACGGACGCTCCTGGGCAGGATCTTTGTCCTAGGTTGCTCCTCAGTCACAGACAGCACTG
TGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTGCCTGTCAGGAGC
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CCGCGGCTGAGACCCTGCAGACGCAGGGAGTCTTAGGAACCATCGTCACCACTCAAAGCC
AGCAGGGCATCTTCTGTACAAAGATCTCCCTGCATATCCACTAGACGGAAGCTGAAGGAA
CGCAACAGCAGAGGAGGCCAACAGACGCCTGGCTGAAGGCTCCGTGGGACCAACGGTGTC
ACCTTCAGAAAAGAGCTGGGAACCTTGAGCAGAGCCGATGGTAACTTCTTGGGGAAAGAAG
GCACCCAGTGAAGTGCATGGTTATTCTGAGTCCTCCTCCTCTGCTTAGTCCCTCTCACTG
TACAGGTCTGTTTCTTCTCGCAGCTGTGGCTGCTGAAGTAGGTCCACTGTGGGGAGAGC
TCATCACAGACTTTGGTTTCGGTTCTGGATTCTCAGTGGTGGCAACCGAGAGTCAGACGAT
ACCCTCTAGGTGAGTCTCAGAGGATCTCTATGCTGTGAGAGGGTTGAGGGCCACCCAGA
ATTTTTTTTTTTTACCAGTTTTTACTGTGCCTGCCCCAGGAGGGAGAATTACTTCCCAGC

FIG. 15B



CTCCACAGCAGCAGGCATGGCTTGCCTCAATGGTCCTGAGATCCCAACAAAACCTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCCTCAGAAGTTGGAGGGTGACTGGACACAG
TTAAGACTCAGAGAGCCAGCTGATAGCTCAAAGCAAAGCATGGCACATACCCACCACCAT
ACCATGGTGCGCATGGGATGGGACAGTTGGAATGTTGCAGATAACGTGTTCTTTTGCCAG
TTCATTTGTTAATAAAATATTTAAACGTTAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCG
G (SEQ ID NO: 42)

FIG. 15C

MEEHGHHEMEGTPLGCHSHIKLLKINREHLVTNIRNTQCLVDNLENGYFSAEDAEIVCA
CPTKPKDKVRKILDLVQSKGEEVSEFFLYVLQQLDAYVDLRLWLSEIGFSPSQLIRTKTI
VNTDPVSRYTQQLRHQLGRDSKFMLCYAQKEDLLEETYMDTLMGLVGFNNENLGS LGGL
DCLLDHSTGVLNEHGETVFVFGDAGVGKSM LLQRLQSLWASGRLTSTAKFFFHFRCRMFS
CFKESDMLS LQDLLFKHFCYPEQDPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPD
SCCPWEPAHPLVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKVLLRGFSPSHLRAY
ARRMFPERTAQEHL LQQLDANPNLCSLCGVPLFCWIIIFRCFQHFQTVFEGSSSQLPDCAV
TLTDVFLLVTEVHLNRPQPSSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLFVFG
QEEVQASKLQEGDLQLGFLRALPDVGPEQGQSYEFFH LTLQAFFTAFFLVADDKVSTREL
LRFFREWTSPGEATSSSCHSSFFSFQCLGGRSRLGPD PFRNKDHFQFTNLFVCGLLAKAR
QKLLRQLVPKAILRRKRKALWAHLFASLSYLKSLPRVQSGGFNQVHAMPTFLWMLRCIY
ETQSQKVGR LAARGISADY LKLAFCNAC SADCSALS FVLH H FHRQLALDLDNNNLNDYGV
QELQPCFSRLTVIRLSVNQITDTGVKVLCEELTKYKIVTFLGLYNNQITDIGARYVAQIL
DECRGLKHLKLGKNRITSEGGKCV ALAVKNSTSIVDVGMWGNQIGDEGAKAF AEALKDHP
SLTTLSLAFNGISPEGGKSLAQALKQNTTTLTVIWLTKNELNDESAECFAEMLRVNQTLRH
LWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRIICF

(SEQ ID NO: 43)

FIG. 16



MEEOGHSEMEGIPLGSHSHIOLKINREILVNTIRNTQCLVDNLLNGYFSAEDAIVCACPTOPDKVRKILDVQSKGEVSEFFLYVL
10 20 30 40 50 60 70 80 90
MEEGHHEMEGTPLGCHSHIKLKKINREHLVNTIRNTQCLVDNLLNGYFSAEDAIVCACPTKPKDKVRKILDVQSKGEVSEFFLYVL 90
NEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACPTQPKDKVRKILDVQSKGEVSEFFLYLL 90

QOLADAYVDLRLLLEIGFSPSLLIOSKVNVNTDPVSRYTOOLRHOLGRDSKFVLCYAKEDLLLEEIYMDTLMGLVGFNLSGLGGL
100 110 120 130 140 150 160 170 180
QCLEDAYVDLRLLSEIGFSPSLLIRTKTIIVNTDPVSRYTOOLRHOLGRDSKFVLCYAKEDLLLEEIYMDTLMGLVGFNLSGLGGL 180
QQLADAYVDLRPWLLEIGFSPSLLTQSKVNVNTDPVSRYTOOLRHHLGRDSKFVLCYAKEBELLEEIYMDTIMELVGFNLSGLSLSL 180

ACLLDHSTGVINEOGETVFLGDAGVGKSMLLQRLQSLWASGRLTAGAKFFHFHRCRMFSCFKESDRLSLODLLFKHFCYEQDPPEEVFA
190 200 210 220 230 240 250 260 270
DCLLDHSTGVINEHGETVFLGDAGVGKSMLLQRLQSLWASGRLTSTAKFFHFHRCRMFSCFKESDMLSLODLLFKHFCYEQDPPEEVFS 270
ACLLDHTTGILNEQGETIFILGDAGVGKSMLLQRLQSLWATGRLLDAGVKFFHFHRCRMFSCFKESDRLCLODLLFKHYCYPERDPEEVFA 270

FLLRFPHVAFITFDGLDELHSDLDLSRVPDSCCPWEPAHPLVLLANLLSGKLLKAGAKLLTARTGVEVPROLLRKKVLLRGFSPSHLRAY
280 290 300 310 320 330 340 350 360
FLLRFPHTALFTFDGLDELHSDFDLSRVPDSCCPWEPAHPLVLLANLLSGRLLKAGAKLLTARTGVEVPROLLRKKVLLRGFSPSHLRAY 360
FLLRFPHVAFITFDGLDELHSDLDLSRVPDSCCPWEPAHPLVLLANLLSGKLLKAGAKLLTARTGIEVPROFLRKKVLLRGFSPSHLRAY 360

ARRMFPERAAQDHLLSQLDANPNLCSLCGVPLFCWIIIFRCFQHFQAAFEQSSQLPDCAVTLTDVLLVTEVHLNRMOPSSLVQNRTRSP
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ARRMFPERALQDRLLSQLEANPNLCSLCVPLFCWIIIFRCFQHFRAAFEGSP-QLPDCTMTLTDVLLVTEVHLNRMOPSSLVQNRTRSP 449

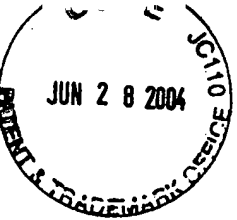
AETLHAGRDTLHALGEVAHRGTDKSLVFQGOEEVOASGLOEGDLOLGLRALPDVPGCGDQSGSYEFFHLLTLOAFFTFFLVADDKVGTOE
460 470 480 490 500 510 520 530 540
AETLRAGWRTLHALGEVAHRGTDKSLVFQGOEEVOASKLOEGDLOLGLRALPDVGPPE-QQGSYEFFHLLTLOAFFTFFLVADDKVGSTRE 539
VETLHAGRDTLCSLQVAHRGMEKSLVFTEEVQASGLQERDMQGLRALPELPGDQDQSGSYEFFHLLTLOAFFTFFLVADDKVGTOE 539

FIG. 17A



	550	560	570	580	590	600	610	620	630	
1. PRO	LLRFFQEWISPGGAASSCHSSFLSFOCLGSGRAGEDLFKNKDHFQFTNLFCVCGILLAKAKOKLLRQLVPAAALRRKRKALWAHLFASLR									
2. PRO	LLRFFQEWISPGGAASSCHSSFLSFOCLGSGRAGEDLFKNKDHFQFTNLFCVCGILLAKAKOKLLRQLVPAAALRRKRKALWAHLFASLR									
3. PRO	LLRFFQEWISPGGAASSCHSSFLSFOCLGSGRAGEDLFKNKDHFQFTNLFCVCGILLAKAKOKLLRQLVPAAALRRKRKALWAHLFASLR									
	640	650	660	670	680	690	700	710	720	
1. PRO	GYLKS LPRVQSGGFNOVQAMPTFLWMLRCIYETOSQKVGOLAARGISADYLLKAFCNACSDCSALSFVLHFFHKOLALDLDNNNNLNDYG									
2. PRO	GYLKS LPRVQSGGFNOVQAMPTFLWMLRCIYETOSQKVGOLAARGISADYLLKAFCNACSDCSALSFVLHFFHKOLALDLDNNNNLNDYG									
3. PRO	GYLKS LPRVQSGGFNOVQAMPTFLWMLRCIYETOSQKVGOLAARGISADYLLKAFCNACSDCSALSFVLHFFHKOLALDLDNNNNLNDYG									
	730	740	750	760	770	780	790	800	810	
1. PRO	VOELQPCFSRLTVLRSLVNOITDGGVKVLSSELTQYKIVTFGLYNNQITDVGARYVAQIILDECKGLTHLSLYNNOITDVGAKLGKKNKIT									
2. PRO	VOELQPCFSRLTVLRSLVNOITDGGVKVLSSELTQYKIVTFGLYNNQITDVGARYVAQIILDECKGLTHLSLYNNOITDVGAKLGKKNKIT									
3. PRO	VOELQPCFSRLTVLRSLVNOITDGGVKVLSSELTQYKIVTFGLYNNQITDVGARYVAQIILDECKGLTHLSLYNNOITDVGAKLGKKNKIT									
	820	830	840	850	860	870	880	890	900	
1. PRO	SEGGKYVALAVKNSTSIDVGMGNQVDEGAKAFAEALKDHPSLTTLTSLASNGISTEGGKSLAQALQONTSLTVLWLTQNELNDEVAES									
2. PRO	SEGGKYVALAVKNSTSIDVGMGNQVDEGAKAFAEALKDHPSLTTLTSLASNGISTEGGKSLAQALQONTSLTVLWLTQNELNDEVAES									
3. PRO	SEGGKYVALAVKNSTSIDVGMGNQVDEGAKAFAEALKDHPSLTTLTSLASNGISTEGGKSLAQALQONTSLTVLWLTQNELNDEVAES									
	910	920	930	940	950	960				
1. PRO	LAEMLKVNQTLKHLWLIQNIITAKGTAQALADALQNSNTGITEICLNGNLKPEEAKVFEDEKRIICE									
2. PRO	LAEMLKVNQTLKHLWLIQNIITAKGTAQALADALQNSNTGITEICLNGNLKPEEAKVFEDEKRIICE									
3. PRO	LAEMLKVNQTLKHLWLIQNIITAKGTAQALADALQNSNTGITEICLNGNLKPEEAKVFEDEKRIICE									

FIG. 17B



tgtatgattctgtttatatgaaatgtccagaaaaggtaaattctatagacaaagcaaattcagtagt
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FIG. 18B



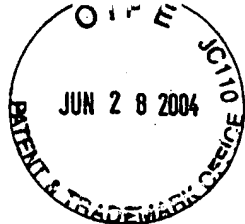
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FIG. 18C



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FIG. 18D



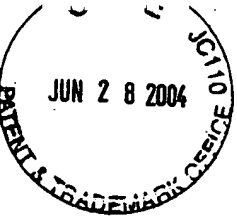
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FIG. 18E



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FIG. 18F



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FIG. 18G



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FIG. 18H



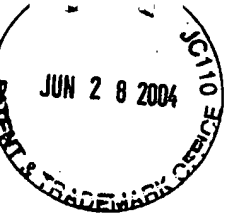
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FIG. 181



tattgtgtgatacacgagtgtgtgctatgaacacaccttgggaaggagtgtgagaggatccttaa
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FIG. 18J



1 GTCGACCCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAGG
CAGCTGGGTGCGCAGGCCGTCCGTCCGACGTCGTCCGCTCGTCCGTCTCTCATTTTCC

63 TGACCGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTT
ACTGGCGCCGACGGGTGGGGTCTCGGTACCCCGCCGTCGTCTACGGTAGGACCTGCGAGAA

1 M G R A R D A I L D A L

125 GAAAACTTGTTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
CTTTTGAACAGTCCCCCTACTTGAGTTTTTCAAGTTCTACTTCGACGACTGTCACGTTGACGC

13 E N L S G D E L K K F K M K L L T V Q L R

187 AGAAGGCTATGGGCGCATCCCACGCGGGGGCCCTGCTGCAGATGGACGCCATAGATCTCACTG
TCTTCCGATACCCGCGTAGGGTGCGCCCGGGACGACGTCTACCTGCGGTATCTAGAGTGAC

33 E G Y G R I P R G A L L Q M D A I D L T

249 ACAAACCTTGTTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCACAATGACTGTGCTTAGA
TGTTTGAACAGTTCGATGATAGACCTCAGCATACCGAACCTCGAGTGTTACTGACACGAATCT

54 D K L V S Y Y L E S Y G L E L T M T V L R

311 GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGAAGAGTCTGGAGCTGT
CTGTACCCGAATGTCCTCGACCGACTCGTCGACGTTTGCTGATTTCTTCTCAGACCTCGACA

75 D M G L Q E L A E Q L Q T T K E E S G A V

373 GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTTGTGGACCAGC
CCGTGACGTCGGTCACAGGGACGAGTCTCATGTCCGTCTTGTCTGTGAAACACCTGGTCCG

95 A A A A S V P A Q S T A R T G H F V D Q

435 ACAGGCAAGCACTCATTTGCCAGGGTCACAGAAGTGGACGGAGTGCTGGATGCTTTGCATGGC
TGTCGGTTTCGTGAGTAACGGTCCAGTGTCTTACCTGCCTCAGCAGCTACGAAACGTACCG

116 H R Q A L I A R V T E V D G V L D A L H G

497 AGTGTGCTGACTGAAGGACAGTACCAGGCAGTTCGTGCAGAGACCACCAGCCAAGACAAGAT
TCACACGACTGACTTCCTGTCATGGTCCGTCAAGCACGTCTCTGGTGGTCCGTTCTGTTCTA

137 S V L T E G Q Y Q A V R A E T T S Q D K M

559 GAGGAAGCTCTTCAGCTTTGTTCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG
CTCCTTCGAGAAGTCGAAACAAGGTAGGACCTTGGACTGGACGTTCTTGAGGGAGGAGGTCC

157 R K L F S F V P S W N L T C K D S L L Q

621 CCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGGAGCAGAGCTGAGGTATCTTTTCC
GGAACTTCCTTTATGTAGGGATGAACCACTACCTGGACCTCGTCTCGACTCCATAGAAAAGG

178 A L K E I H P Y L V M D L E Q S

683 AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTTTTGAAAAACAATTTGTATTGT
TCGATGTAATAGATCGAGGACTGAAACATATGTGTTAAAACTTTTTTGTAAACATAAACA

745 GTTTAAAAAAGGGCGGCGC
CAAAATTTTTTTTTTTTTTTTCCCGCGGCGC

FIG. 19

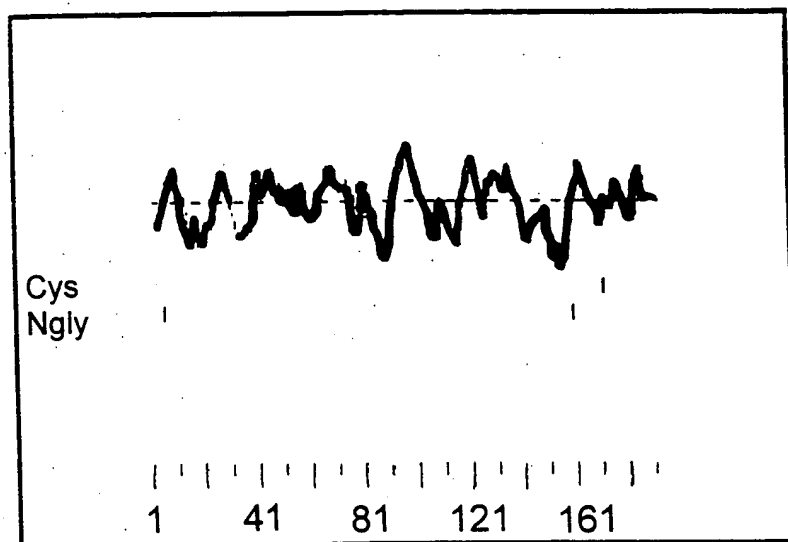


FIG. 20

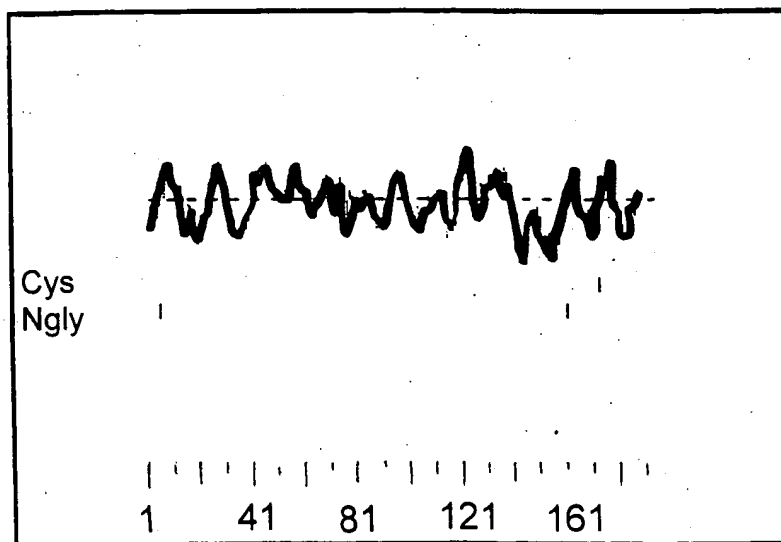


FIG. 22



1 CGCGTCCGGCTGCAGCGGGGTGAGCGGCGGCAGCGGCCGGGGATCCTGGAGCCATGGGGC
GCGCAGGCCGACGTGCGCCCACTCGCCGCGGTGCGCGGCCCTAGGACCTCGGTACCCCC

1► M G

61 GCGCGCGCGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGT
CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGACTGGCGGCTCCTCGAGTTCTTCA
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTGCGGTGCCGCTGCGCGAGGGCTACGGGCGCATCCCGCGGGGCG
AGTTTCGACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCCCGCGTAGGGCGCCCCGC
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGAACGCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA
GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTCGACCAGTCGAAGATGGACCTCT
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCGACATGGGCCTGCAGGAGATGGCCG
GGATGCCCGCGGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGGACGTCTCTACCGGC
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGCCACGCACCAGGGCTCTGGAGCCGCGCCAGCTGGGATCCAGGCCC
CCGTGACGTCCGCGCGGTGCGTGGTCCCGAGACCTCGGCGCGGTGACCCCTAGGTCCGGG
83► G Q L Q A A T H Q G S G A A P A G I Q A

361 CTCCTCAGTCGGCAGCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA
GAGGAGTCAGCCGTCCGTTCCGTCGCGACGTGAAATATCTGGTCGTGGCCCGACGCGAAT
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCCTGACGG
AGCGCTCCCACTGTTTGCAACTCACCGACGACCTACGAGACATGCCCTTCCAGGACTGCC
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAGGCAGTGCAGGCGGAGCCCAACCAAGCAAGATGCGGAAGCTCT
TACTCGTCATGGTCCGTCACGCCCCGGCTCGGGTGGTTGGGTTCTTACGCCCTTCGAGA
143► D E Q Y Q A V R A E P T N P S K M R K L

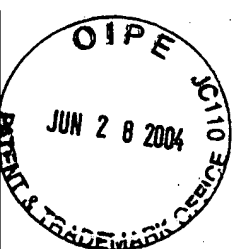
541 TCAGTTTCACACCAGCCTGGAAGTGGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG
AGTCAAAGTGTGGTCGGACCTTGACCTGGACGTTCTGAACGAGGAGGTCCGGGATTCCC
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCAGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCCAGCAACAC
TCAGGGTACGATGGACCACTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCGTTGTG
183► E S Q S Y L V E D L E R S

661 TCCGGTCAGCCCTGGCAATCCCAACCAATCATCCTGAATCTGATCTTTTTATACACAAT
AGGCCAGTCGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTTA

721 ATACGAAAAGCCAGCTTGAA
TATGCTTTTCGGTCGAACCTT

FIG. 21



ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

> hCARD5-DNA 740 aa vs.
> mCARD5-DNA 763 aa

scoring matrix: paml20.mat, gap penalties: -12/-4

68.2% identity; Global alignment score: 2377

```

      10      20      30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :  ::::::::::: :::: :  :::: :::::  ::
      CCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGCAGCAGCAGCAAGAGTAAAAGGTGAC
      10      20      30      40      50      60

      40      50      60      70      80      90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGACGCCATCCTGGATGCGCTGGA
      :: :: :  :: ::::::::::: ::::: ::::::::::: :::::
      CGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTTGA
      70      80      90      100     110     120

      100     110     120     130     140     150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTGCGGTGCCGCTGCG
      :::: :::: :  :: ::::::::::: ::::::::::: :::::
      AAACTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
      130     140     150     160     170     180

      160     170     180     190     200     210
inputs CGAGGGCTACGGGCGCATCCCGCGGGGCGCGCTGCTGTCCATGGACGCCTTGGACCTCAC
      ::::::::::: ::::::::::: ::::: :::::  ::::::::::: :::::
      AGAAGGCTATGGGCGCATCCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
      190     200     210     220     230     240

      220     230     240     250     260     270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCGCTAAC-GTGC
      ::::: ::::: ::::: ::::: :  ::::: ::::: :  :::::
      TGACAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
      250     260     270     280     290

      280     290     300     310     320     330
inputs TCGCGGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
      :  ::::::::::: ::::: ::::::::::: :  :::::
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
      300     310     320     330     340     350

      340     350     360     370     380     390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCCTGC
      ::::: :  ::::: :  ::::: :  ::::: :  ::::: :  :::::
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
      360     370     380     390     400     410

      400     410     420     430     440     450
```

FIG. 23A



ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hCARD5-protein 195 aa vs.
> mCARD5-protein 193 aa
scoring matrix: paml20.mat, gap penalties: -12/-4
71.8% identity; Global alignment score: 712

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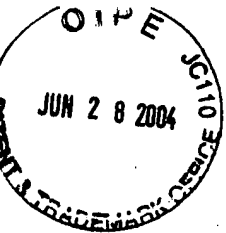
      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSFY
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVQLREGYGRIPRGALLQMDAIDLTDKLVSY
      10      20      30      40      50      60

      70      80      90      100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA
      .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90      100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQA
      .....
      ALIARVTEVDGVLDAHGSVLTEGQYQAVRAETTSQDKMRKLFSFVPSWNLTCKDSSLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS
      .....
      LKEIHPYLVMDLEQS
      180     190
```

FIG. 24



1 CCCGCGTCCGGAAGTTCCTTCCAGTGTGTTGTTCTCTCTGCTCTCTCCAACAGAAGGTATTTTTG
GGGCGCAGGCCTGAAGGGAAGGTCACAAACAAGGAGAGACGAGAGAGGTTGTCTTCCATAAAAAC

66 GCATGTTTTATCTTTGCTAAGTAGGATTTCTGTCTTTCTTTGTTAAACACAGATTTCTTTCTGTGC
CGTACAAAATAGAAACGATTTCATCTTAAGACAGAAAGAAACAATTGTGTCTAAAGAAAGACAGC

131 CAGAATGACCTGATCCATTTCTGGTTTTGTAGAAAGCCATGGCTTCAGAGGGTGCTTCCTCAGAA
GTCTTACTGGACTAGGTAAAGGACCAACATCTTTCCGTACCGAAGTCTCCCACGAAGGAGTCTT

1 M A S E G A S S E

196 ATCATAGAAAAACAGCGAACAAAGTTGCTCAGTGTCTCCAACAAGATCCCGACTCTATCTTGA
TAGTATCTTTTTGTGCGTTGTTTCAACGAGTCACAGGAGGTGTCTTAGGGCTGAGATAGAACCT

10 I I E K Q R T K L L S V L Q Q D P D S I L D

261 CACGTTAACCTCTCGGAGACTGATTTCTGAGGAGGAGTATGAGACTCTAGAGGCAATTACAGATC
GTGCAATTGGAGAGCCTCTGACTAAAGACTCCTCCTCATACTCTGAGATCTCCGTTAATGTCTAG

31 T L T S R R L I S E E E Y E T L E A I T D

326 CTCTGAAGAAAAGCCGGAAGCTGTAAATTTTGATCCAGAAGAAGGGAGAGGACAGCTGTTGTGT
GAGACTTCTTTTCGGCCTTCGACAATTAATACTAGGTCTTCTCCCTCTCCTGTGACAACAACA

53 P L K K S R K L L I L I Q K K G E D S C C C

391 TTCCTCAAGTGTCTGTCTAATGCCTTTCCACAGTCAGCTTCCACCTTGGGTTTAAAGCAGGAAGT
AAGGAGTTACAGACAGATTACGGAAGGTGTGAGTCGAAGGTGGAACCCAAATTTCTGCTCTCA

75 F L K C L S N A F P Q S A S T L G L K Q E V

456 TCCACGGCAGGGGACTGGAGAGGTTGTGAGGTGAGCAGGGGTTTGAAGATCCCTTTTCTCTTG
AGGTGCCGTCCCCTGACCTCTCCAACAGCTCCACTCGTCCCCAACCTTCTAGGGAAGAGAAAC

96 P R Q G T G E V V E V S R G L E D P F S L

521 GGACCATAACCCAGAAAATAGCAGAGCTCTCAGAAGAGAAAGAATGCCCGGGTCTGGGAGCTCCG
CCTGGTATTGGGGTCTTTATCGTCTCGAGAGTCTTCTCTTTCTTACGGGCCAGACCTCGAGGC

118 G T I T P E I A E L S E E K E C P G L G A P

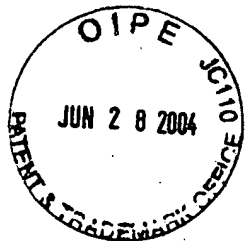
586 GAGTTCTTACCTGCAAGGAAAGCAGCCACAGGGAACCGGAAGTACCTTCTTGGGAGAATCAGGA
CTCAAGAAGTGGACGTTCTTTTCGTGCGGTGTCCCTTGGCCTTCATGGAAGAACCCTCTTAGTCCT

140 E F F T C K E S S H R E P E V P S W E N Q E

651 AGGGCGTGGTGCACAGCAAGTCACCGCTCCGCGTTTCAAGGAGTTGAGTATGAAGTTCCAG
TCCCGCACCACGTGTGTTTCAAGTGGCGAGGCGCAAGTCAGTTTCTCAACTCATACTTCAAGGTC

161 G R G A Q Q V T A P R S V K G V E Y E V P

FIG. 25A



716 CAAGTATCTCCCTCTTAAGCGACGGGCAGAGATACGAGGAGCCAGATGATTCCGCTGTACTTAGAA
GTTTCATAGAGGGAGAATTTCGCTGCCCCGTCTCTATGCTCCTCGGTCTACTAAGCGACATGAATCTT

183▶ A S I S L L S D G Q R Y E E P D D S L Y L E

781 GAAGGGGAAGGTGAAGAGTCTCTTGGGTACCCCTGAAGATGTTTTGGAGGAAGGGGCCGCGATGA
CTTCCCCCTTCCACTTCTCAGAGAACCCATGGGACTTCTACAAAACCTCCTTCCCCGGCCGCTACT

205▶ E G E G E E S L G Y P E D V L E E G A G D D

846 CCCACAGTGCTTTGTATATGATAGTGAGGAGGAATGCCAGTATGAGGAAAACATGGGCTCCTCCG
GGGTGTCACGAAACATATACTATCACTCCTCCTTACGCTCATACTCCTTTTGTACCCGAGGAGGC

226▶ P Q C F V Y D S E E E C E Y E E N M G S S

911 GTGAAGACAGTAGCTGCGACGACACTTCAGAGACCTGCGTTCCATTGGAAGGGGAGAAAAGCGCT
CACTTCTGTGTCATCGACGCTGCTGTGAAGTCTCTGGACGCAAGGTAACCTTCCCCTCTTTTCGCGA

248▶ G E D S S C D D T S E T C V P L E G E K S A

976 GAAGAAAGAAAAAGAGTGTTTTCAACACGTCCTGTCTCTGTTTGAACATGGATAGAAACAGAAAGCT
CTTCTTTCTTTTCTCACAAGTTGTGCAGGACAGGACAACTTGTACCTATCTTTGTCTTTTCCA

270▶ E E R K R V F Q H V L S C L N M D R N R K L

1041 TCTCCCAGAGTTCGTGAGGCAGTTTTTCCATAGACCGAGGATGTGAGTGGACACCCAAGACCCCAG
AGAGGGTCTCAAGCACTCCGTCAAAGGTATCTGGCTCCTACACTCACTGTGGGTTCTGGGGTC

291▶ L P E F V R Q F S I D R G C E W T P K T P

1106 GAGACTTAGCTTGAATTTCTTGATGAAAGTTCAGGCTTTAGACTCGACAGCCAGAGATTCTATC
CTCTGAATCGAACCTTAAAGAACTACTTTCAAGTCCGAAATCTGAGCTGTGGTCTCTAAGATAG

313▶ G D L A W N F L M K V Q A L D S T A R D S I

1171 CTGAGGCCCGAGGTGGCGGGTGAAGAGAATGAAGAATTGCCGGCTGGAATAGAGAAGTTAGGCAT
GACTCCGGGCTCCACCGCCCACTTCTCTTACTTCTTAACGGCCGACCTTATCTCTTCAATCCGTA

335▶ L R P E V A G E E N E E L P A G I E K L G I

1236 TGGAGACCCCCAAACCATCCATCCCCTGGATGTCCTCTGCGCCTGCATGCTTTGTGCAGACAGCT
ACCTCTGGGGGTTTGGTAGGTAGGGGACCTACAGGAGACGCGGACGTACGAAACACGTCTGTCTGA

356▶ G D P Q T I H P L D V L C A C M L C A D S

1301 CCTTGCAGCGTGAAGTCATGTCAAACATGTACCAATGCCAGTTTGTCTTCCCCTGCTACTGCCA
GGAACGTTCGCACTTCAGTACAGTTTGTACATGGTTACGGTCAAACGAGAAGGGGACGATGACGGT

378▶ S L Q R E V M S N M Y Q C Q F A L P L L L P

1366 GATGCTGAGAACAACAAAAACCTCTTAATGGTAGGGGCCATGAAGGACTTAAAGCAGCCCTCAGC
CTACGACTCTTGTGTGTTTTGGAGAATTACCATCCCCGGTACTTCTGAAATTCGTGGGGAGTCCG

400▶ D A E N N K N L L M V G A M K D L K Q P S A

FIG. 25B



1431 ACAGTCCTCAGGAGGGCCCCCTCAGGGAAACAGACACATTTCTGGGTCTCACAAAGATGCCTGTCA
TGTCAGGAGTCCCTCCCGGGAGTCCCTTTGTCTGTGTAAAGACCCAGAGTGTCTTACGGACAGT
421▶ Q S S G G P L R E T D T F L G L T K M P V

1496 TCTCTTTTGTGCGACTAGGACGCTGCAGCTTCTCCAAGTCCAGAATTGTTAACACACTGCTCAGC
AGAGAAAACACGCTGATCCTGCGACGTGGAAGAGGTTCAAGTCTTAACAATTGTGTGACGAGTCTG
443▶ I S F V R L G R C S F S K S R I V N T L L S

1561 TCCTCCCAGCAGAAACCATACCCGATTTTCTCCATCAGGATCTGTCTGTCCCTGTGCTTCTCTG
AGGAGGGTCTGCTTTTGGTATGGGCTAAAAGGAGGTAGTCTTAGACAGACAGGGACACGAAGGAGC
465▶ S S Q Q K P Y P I F L H Q D L S V P V L P R

1626 GCAAATTTCTGACGGCCTGGTGAAGTGACATGGTGCTTTCTGACAAGTTGCTGAAGGAAAGCC
CGTTTAAAGACTGCCCGACACCTTCACTGTACCACGAAAGGACTGTTCAACGACTTCTTTTCGG
486▶ Q I S D G L V E V T W C F P D K L L K E S

1691 CGCATGCTTTCCAGAAACCTGTGTGCTGTGGCCAACCTTCGTGGAGATTTAGAAAGCTTTTGGATA
GCGTACGAAAGGTCTTTGGACAACGACACCGGTTGGAAGCACCTCTAAATCTTTGAAAACCTAT
508▶ P H A F Q K P V A V A N L R G D L E S F W I

1756 CAATTTGGTTTCTCTGGTAGAAGTTTCTCCGGTCTTTTCTTTTTCACAGACTGCCTTGGTGAGAA
GTTAAACCAAAGGACCATCTTCAAAGGAGGCCAGAAAAGAAAAAGTGTCTGACGGAACCACTCTT
530▶ Q F G F L V E V S S G L F F F T D C L G E K

1821 GGAATGGGACTTGCTAATGTTTTTAGGAGAGGACACCATTGAACGGTGCTACTTTATCCTCAGTC
CCTTACCCTGAACGATTACAAAAATCCTCTCTGTGGTAACTTGCCACGATGAAATAGGAGTCAG
551▶ E W D L L M F L G E D T I E R C Y F I L S

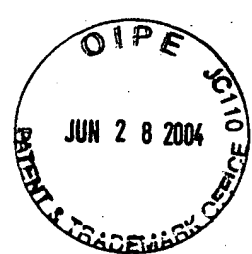
1886 CCCAGGCTAAGGAGAGTGAAGAAGCCCAGATTTTCCAAAGGATCCTAAAACTGAAGCEATCTCAG
GGGTCCGATTCTCTCACTTCTTCGGGTCTAAAAGGTTTCTTAGGATTTTGACTTCCGTAGAGTC
573▶ P Q A K E S E E A Q I F Q R I L K L K P S Q

1951 CTACTGTTTTGGGAAGCTGAGGAAGCTGGGGATAGAAGGAAGACTATGGAGGCCCTTCAAGCTGC
GATGACAAAACCTTCGACTCCTTCGACCCCTATCTTCTCTGATACCTCCGGGAAGTTCGACG
595▶ L L F W E A E E A G D R R K T M E A L Q A A

2016 CCTCCAGGAAGTAATGTCCTCTCCACTCAGATGTGTGTCCCTTGAAGAGATGGCCTCTCTGGCCA
GGAGGTCCTTCATTACAGGAGAGGTGAGTCTACACACAGGGAAGTCTCTACCGGAGAGACCGGT
616▶ L Q E V M S S P L R C V S L E E M A S L A

2081 GGGAGCTGGGCATTTCAGGTAGACCAAGACTTTGAAGTTACTCAAGATATTCAAGTTTCCCCACA
CCCTCGACCCGTAAGTCCATCTGGTTCTGAAACTTCAATGAGTTCTATAAGTTCAAAGGGGTGT
638▶ R E L G I Q V D Q D F E V T Q D I Q V S P T

FIG. 25C



2146 ACAGTTGAAGGTGAAAACCAACAACCATGTAGTCAGACCAAAGCCCGGCTGAAAGCGGAGCTCA
TGTCAACTTCCACTTTTGGTTGTTGGTACATCAGTCTGGTTTTCGGGCCGACTTTCGCCCTCGAGT
660▶ T V E G E N Q Q P C S Q T K S P A E S G A Q

2211 GGAGCCAATCAGAGAGCCAGGGGCTCAATGTGACGACAGTCAGAATGCTCCGGTTTTCATCAGA
CCTCGGTTAGTCTCTCGGTCCCCGAGTTACACTGCTGTCTAGTCTTACGAGGCCAAAAGGTAGTCT
681▶ E P I R E P G A Q C D D S Q N A P V F H Q

2276 CTCCAGTATACATGCCTTATCCAGCACACCCATGGGCTTTGGCCATCAAAGCTGGAGGTAACTTT
GAGGTACATGTACCGGAATAGGTCTGTGGGTACCCGAAACCGGTAGTTTCGACCTCCATTGAAA
703▶ T P V Y M P Y P A H P W A L A I K A G G N F

2341 TACCACGTTCCCTTTGAATGCCCCCTGGTTATGGGCTCCCACTTTGGATCACAGCAGAGGGCTAAG
ATGGTGCAAGGAACTTACGGGGGACCAATACCCGAGGGTGAAACCTAGTGTCTCTCCCGATTCT
725▶ Y H V P L N A P W L W A P T L D H S R G L S

2406 TGGTTCTTTCCATTCCCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAACTGCCACCATC
ACCAAGAAAGGTAAGGGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTGATTGACGGTGGTAG
746▶ G S F H S H A K P T H S K A F Q A N C H H

2471 CCCATCCCTCCCATGCTAAACCCACTCATGTGAATCCCTCTCATGCTAACCCCACTCATGTGCAG
GGGTAGGGAGGGTACGATTTGGGTGAGTACACTTAGGGAGAGTACGATTGGGGTGAAGTACACGTC
768▶ P H P S H A K P T H V N P S H A N P T H V Q

2536 CCTTGCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAAACCCACTCCCTCTCAGACCTCT
GGAACGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTGATTGAGGTGAGGGAGAGTCTGGAGA
790▶ P C M L N P L T L R P S K L N P L P L R P L

2601 TGGAGCCAAGCTAACTGCAATCATGCCCATCCCTCCCTTGCTAAACCCCTCTCATACGAATCCCTC
ACCTCGGTTGATTGACGTTAGTACGGGTAGGGAGGGAACGATTTGGGAGAGTATGCTTAGGGAG
811▶ G A K L T A I M P I P P L L N P L I R I P

2666 TGATGCTAACCCCACTCATGTGCAGCCTTCCCATGCTAAACCCGCTCATCTACAGTCTTCCCAA
ACTACGATTGGGGTGAGTACACGTCGGAAGGGTACGATTTGGGCGAGTAGATGTCAGAAGGGTTT
833▶ L M L T P L M C S L P M L N P L I Y S L P K

2731 CAAAACCTCCCCATCCCAATCTACTGCAGTTTACGGCACACAAACCTCAGCAGTCCCAGTCTAA
GTTTTGGGAGGGGTAGGGTTAGATGACGTCAAGTGCCGTGTGTTGGAGTCGTCAGGGTCAGATT
855▶ Q N P P H P N L L Q F T A H K P Q Q S Q S K

2796 GCCTTCTCAGCAGAGACCCAGTCAGCCTAAATCATTCCAGACCAAGCCTTCACAGGCCAGGGCCT
CGGAAGAGTCGTCTCTGGGTCAAGTCGATTTAGTAAGGTCTGGTTCGGAAGTGTCCGGTCCCGGA
876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

FIG. 25D



2861 GCCACCCAAGAGCAGGGAGACGTTAAAGAACATACTCTGGAGATCTGGGAAATAAAGTATGGGCT
CGGTGGGTTCTCGTCCCTCTGCAATTTCTTGATGAGACCTCTAGACCCTTATTTTCATACCCGA

898 C H P R A G R R

2926 TTGCTTAAGTATTCTTTTTTCATATAGCAAGCTGAAGAAAAGTTTTAGTGAAAGACTGATAAAAGT
AACGAATTCATAAGAAAAGTATATCGTTTCGACTTCTTTTCAAAATCACTTTCTGACTATTTTCA

2991 AGCAAAACCCAAAAAGGTATGCAAAGTCTTAAGTGCATAGCAAAGTATCCAAGTGTGGGAAATA
TCGTTTTGGGTTTTTTCATACGTTTCAGAATTCACGTATCGTTTCATAGGTTACACCCCTTTAT

3056 TGGAAGCAGTTAAAAGTAGAATCTGGCTGGGCATGGTGGCACACATCTACAGGGTTTACGATGGG
ACCTTCGTCAATTTTCATCTTAGACCGACCCGTACCACCGTGTGTAGATGTCCCAAATCGTACCC

3121 AGGGCTCTGTCATCCCAACTCAGAGAAGCAGGCAGATCTCTGTGTGTTTGAGGCCAGTCTGGTCT
TCCCGAGACAGTAGGGTTGAGTCTCTTCGTCCGTCTAGAGACACACAACTCCGGTCAGACCAGA

3186 ACATAACAACGACACAAGCAAGTCCTACATCAGCCATACTACAAAATGAGACCCCATCTGGGGAC
TGTATTGTGCTGTGTTTCGTTTCAGGATGTAGTCGGTATGATGTTTTACTCTGGGGTAGACCCCTG

3251 AAAAGGGTTGGATCTAACATCAAACCAAAGAAATCAGTCAAGTATTCAGAAGGCATCATTAAAT
TTTTCCCAACCTAGATTGTAGTTTGGTTTCTTTAGTCAGTTCATAAGGTCTTCCGTAGTAATTAA

3316 ACACTCAGTGGGTTACCACAACCAAACCATCTCGACAACCTAACCCCTAAAGGAGCAAGAAGGA
TGTGAGTCACCCAATGGTGTGGTTTGGTATGAGCTGTTGATTGGGGGATTTCTCGTTCTTCCT

3381 GTTGGGTGGGTGTTAGGCTGAACATGATTGGGGAAGAACTGAAGATAGATAAGGTCAATTCGTAAT
CAACCCACCCACAATCCGACTTGTACTAACCCCTTCTTGACTTCTATCTATTCCAGTAAGCATTAA

3446 ACAGGTTATGGGACTTGTCAAATCCATTAAATGCAATATTAAGAAGCAGTGGGAATCTTAAGGCT
TGTCCAATACCTGAACAGTTTAGGTAATTTACGTTATAATTCTTCGTCACCCTTAGAATTCCGA

3511 ACATTAAGCTCCAGTGAGTCGCAACCCCTCCCCTATTAGATGATGTGAGATTTGAACCCCAAGTGAA
TGTAATTGAGGTCACCTCAGCGTTGGGAGGGGATAATCTACTACACTCTAAACTTGGGGTCACCT

3576 TGGGGTGTGCTGATAGCCCGTGTGTGTGACAACTGTGTAATTATAAAGTGATGAAAACGTGGG
ACCCACACAGACTATCGGGCACACACTGTTTGACACATTAAATTTCACTACTTTTGCACCC

3641 AGTTCAGCTTATCTGTGTTGAAGAAAGGCTGCTTCAGAGGTGCCTTGGTTTTGGGTTTATGATCA
TCAAGTCGATAGACACAACCTCTTTCCGACGAAGTCTCCACGGAACCAAAACCCAAATACTAGT

FIG. 25E



3706 GCCACTGAGCAGATACTCTGCACCATTTGGTACAGTTAAATCAGCTTGCTTCTGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCATGTCAATTTAGTCCAACGAAGACCATTTATCGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATAATGAATGATCAGCAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCTTTATTACTTACTAGTCGTTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTTGTATATGTATCATTTCTTTATATAATAGCTAAGAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCTTTTAAATCGAGTAA

3901 AGGGGTTCTGATATATTAGTTTTAATGGTTTGAAGTCAGAAATGTGTTAGTTTTTAAATTTTAGAGT
TCCCCAAGACTATATAATCAAATTACCAAACCTTCAGTCTTTACACAATCAAAAATTTAAATCTCA

3966 TAATTGAAAATATTGAGATGAATTTACAAAGGCTATAAGTAATGTTTGAGAGGGTTATAATTTTT
ATTAACTTTTATAACTCTACTTAAATGTTTCCGATATTCATTACAACTCTCCCAATATTAAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAACCTATCGAAGAGCATCAATCGTCACAATATCTTCTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTTTAAGTGTACCAAGAGTCAATAAAG
TAAACTAAGTCCATAAATTGGTCTCGACGAGAAATCAAAAATTCACAGTGGTTCTCAGTTATTTTC

4161 GCTACATTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCCTTGTGTTGACACTGGAATGTGAATTCCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCATAGTGAGACCAGGTCTCAAGACACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCTCGTGTATCACTCTGGTCCAGAGTTCTGTGTTTTTGATAGGTGGAAT

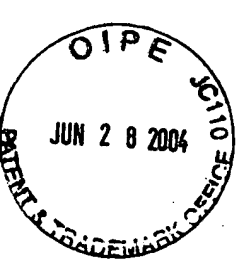
4291 AGGAAGATTTTTAAATTTGCCTCATTAAGAAATAAAGTAAGATTTATAAATTGGACTAAATGTCA
TCCTTCTAAATTTTTAAACGGAGTAATTCCTTTATTTCATTCTAAATATTTAACCTGATTTACAGT

4356 CATCTTTGAACTTATGACTGTTTAATTTTTTGACTTAAAGTTTAATTTTATTATGTATGCGTGT
GTAGAACTTGAATACTGACAAATTAAAAAAGTGAATTTCAAATTAATAACATACGCACA

4421 GTTGATGTGTGTGCACATGTGTGCCACTGCATGTATGTGGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACACGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTACAACATCTC

4486 TCTGTTCTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAATCGGGATACACAAAATGGGTGACTCGATCCGGTGGATGAGGATATTCAG

FIG. 25F



4551 TAATTTTAAATAGTAAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAAAATTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTMTTACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAATCATTTGTGTCTGAGAATAGCC
TTCTTTTTTAGCATAATCGGTACCTATCTCTGAGTGGAGAACTTAGTAAACACAGACTCTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTGTATTATACACAAACATGTACACAATCAATTATAACAAAAGTCTCATAAATTAGAGAG

4746 ATGATTATTGTAAAGATGAAAAAAGAAATAGTGGGCAATGTATGTGAGTATTTAATTTTGCTGA
TACTAATAACATTTCTACTTTTTCTTTTATCACCCGTTACATACACTCATAAATTAAACGGACT

4811 CAATTCTGTCTTTTAGAATGATAAATGTAAAGTAAAATAAAACGGTTTCATTCTCAGAACAACT
GTTAAGACAGAAAATCTTACTATTTACATTCCTTCATTTTATTTTGCCAAGTAAGAGTCTTGTGA

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCGGTCGAGTGAATTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAATGACTGAGTCAAGCTTGCCTAATGACTTTTGGACATAAAGTTTATG
TTTCAAATCTCTTCTTTTACTGACTCAGTTCGAACGGATTACTGAAAACCTGTATTTCAAATAC

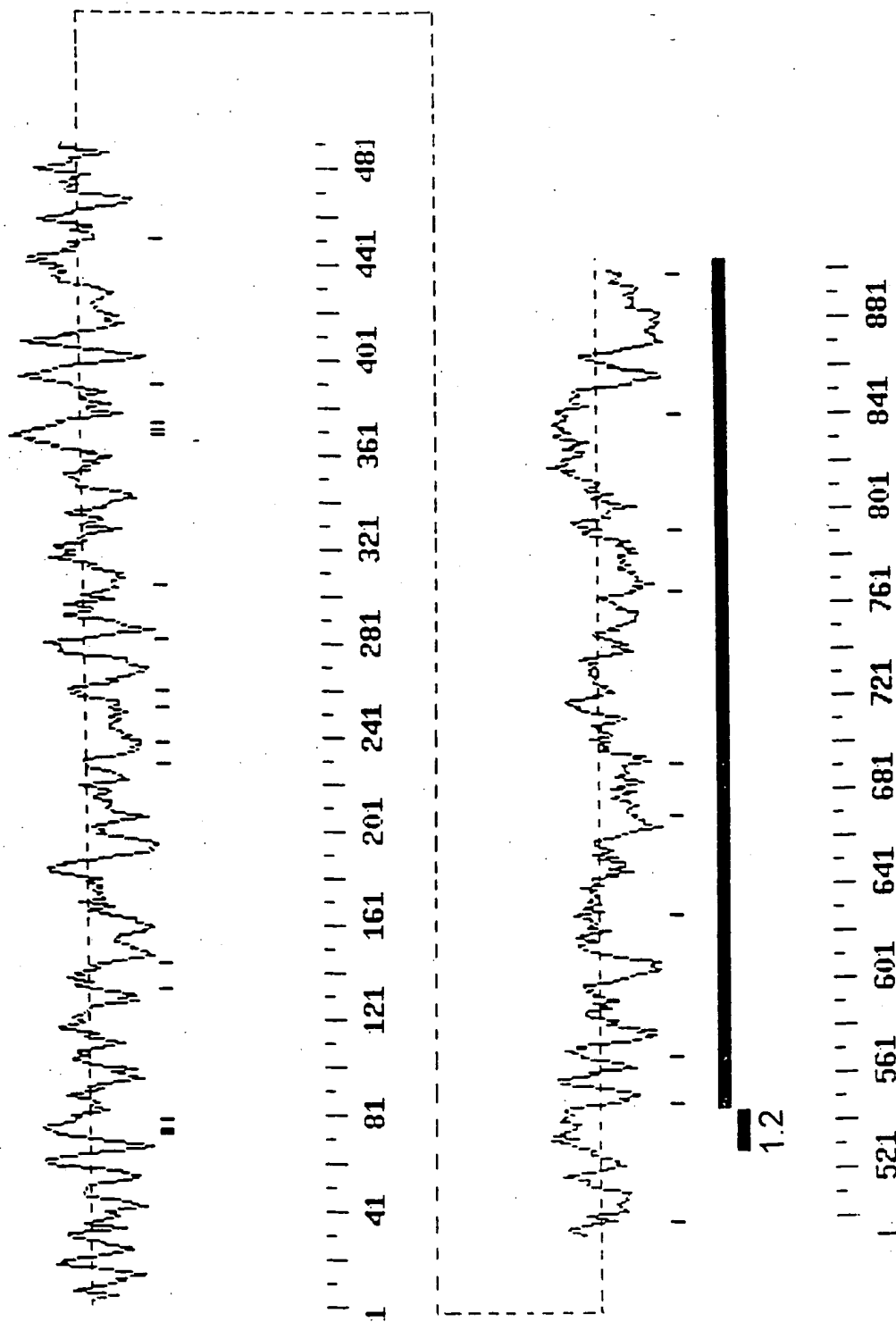
5006 GTCCTAGAAAGCCTTAAAATAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTTCGGAATTTTATTCATCCTATATTTGTACATTTAATTGGGTGTGTAATACACCCA

5071 TGAGAAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTC
ACTCTTCGTCTTTTTACAGTCATCTTGTGAGCCGGTCACGTATTTCTTCCTTCTCTGGAGACAAG

5136 TGGGTTATAAAACTGCTCTTTGTGCTCAATTTGTCCCTGCTTTTGTGTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAACAAACGGTCTTACATGTTCT

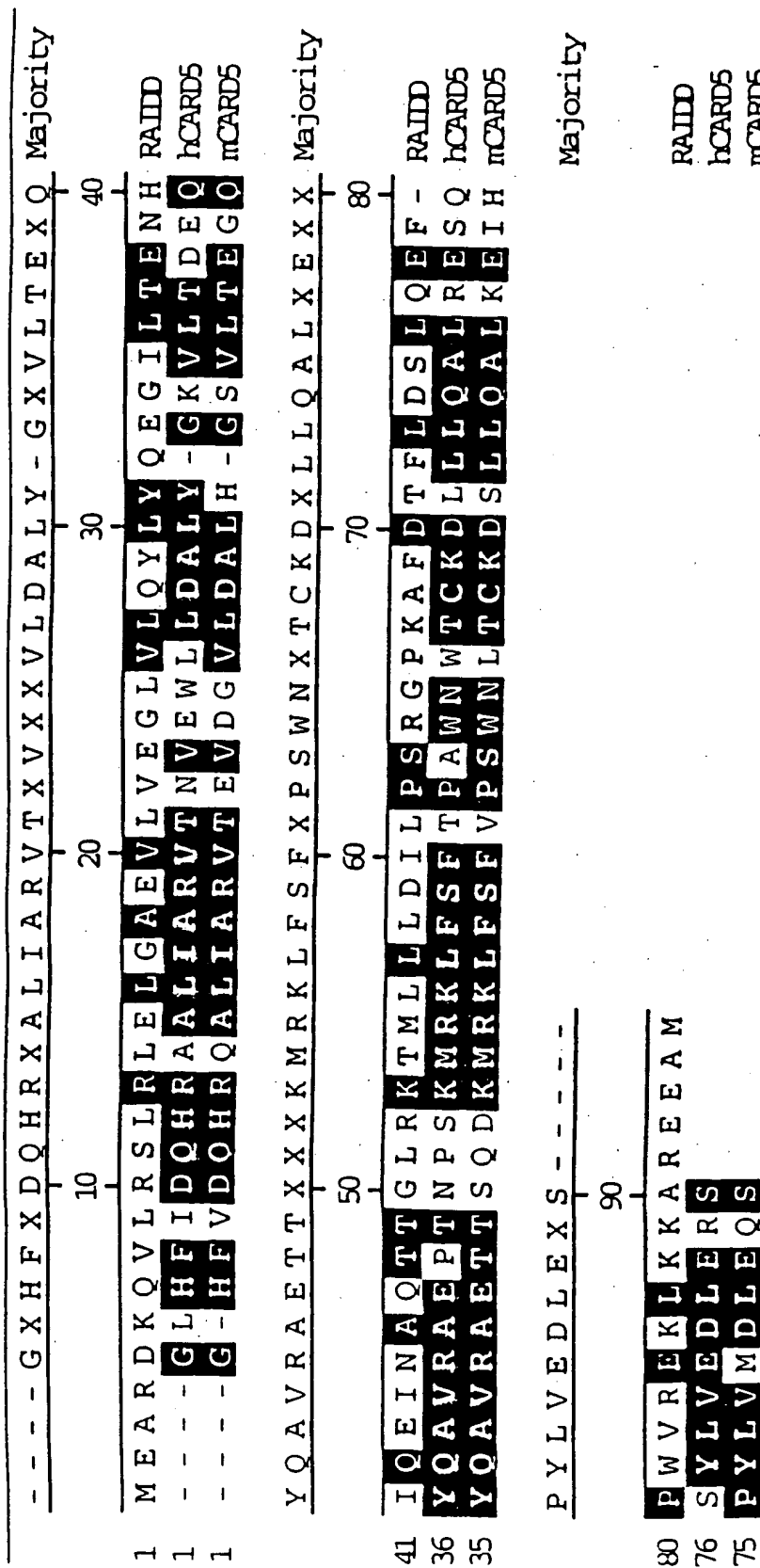
5201 TTATAAAATAAACTCACTTTTACTTTTAAAAAAGGGCGG
AATATTTTATTTGAGTGAAAATGAAAATTTTTTTTTTTTTTTTCCCGCC

FIG. 25G



Cys
out
TM
ins

FIG. 26





CACGCGTCCGCCGATCAGAGAGTGCTCCGAGCTGGGTTGCCCCACTGTGCTTGATCTGCACTCTCCAACACTAGGC 79
ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTTCTTGTGTCATTCTTTTTTAACTTTTACTTATTCATTAGGAT 158
M A T E S T P S E 9
GATTTCATAATATATTCTCTGGTTTAGAGGAAACAGGAACA ATG GCT ACC GAG AGT ACT CCC TCA GAG 226
I I E R E R K K L L E I L Q H D P D S I 29
ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286
L D T L T S R R L I S E E E Y E T L E N 49
TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346
V T D L L K K S R K L L I L V Q K K G E 69
GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406
A T C Q H F L K C L F S T F P Q L A A I 89
GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466
C G L R H E V L K H E N T V P P Q S M G 109
TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526
A S S N S E D A F S P G I K Q P E A P E 129
GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586
I T V F F S E K E H L D L E T S E F F R 149
ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646
D K K T S Y R E T A L S A R K N E K E Y 169
GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706
D T P E V T L S Y S V E K V G C E V P A 189
GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766
T I T Y I K D G Q R Y E E L D D S L Y L 209
ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826
G K E E Y L G S V D T P E D A E A T V E 229
GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886
E E V Y D D P E H V G Y D G E E D F E N 249
GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946
S E T T E F S G E E P S Y E G S E T S L 269
TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006
S L E E E Q E K S I E E R K K V F K D V 289
TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066
L L C L N M D R S R K V L P D F V K Q F 309
CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126
S L D R G C K W T P E S P G D L A W N F 329
TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186
L M K V Q A R D V T A R D S I L S H K V 349
CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246
L D E D S K E D L L A G V E N L E I R D 369
CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

FIG. 28A



I Q T I N P L D V L C A T M L C S D S S 389
ATA CAA ACC ATT AAT CCC CTT GAC GTG CTT TGT GCC ACC ATG CTG TGT TCA GAT AGC TCT 1366

L Q R Q V M S N M Y Q C Q F A L P L L L 409
TTG CAA CGC CAA GTC ATG TCA AAC ATG TAT CAG TGC CAG TTT GCT CTT CCC CTG CTA CTG 1426

P D A E N N K S I L M L G A M K D I V K 429
CCA GAT GCA GAA AAC AAC AAA AGC ATC TTA ATG CTG GGG GCC ATG AAA GAC ATT GTG AAG 1486

K Q S T Q F S G G P T E D T E K F L T L 449
AAG CAG TCA ACA CAG TTT TCA GGG GGG CCT ACA GAG GAT ACA GAA AAG TTT CTG ACT CTC 1546

M K M P V I S F V R L G Y C S F S K S R 469
ATG AAG ATG CCT GTC ATC TCT TTT GTG CGT CTA GGA TAC TGT AGC TTC TCT AAG TCC AGA 1606

I L N T L L S P A Q L K L H K I F L H Q 489
ATC CTC AAC ACA CTT CTC AGC CCT GCC CAG TTG AAA TTA CAC AAA ATC TTT CTT CAT CAA 1666

D L P L L V L P R Q I S D G L V E I T W 509
GAT TTG CCT CTT TTG GTG CTT CCC CGG CAA ATC TCT GAT GGC CTG GTT GAG ATA ACA TGG 1726

C F P D S D D R K E N P F F Q K P V A L 529
TGT TTT CCT GAT AGC GAT GAT AGA AAG GAA AAC CCC TTT TTC CAA AAG CCT GTT GCT CTG 1786

A N L R G N L E S F W T Q F G F L M E V 549
GCT AAT CTC CGT GGA AAT CTA GAA AGT TTT TGG ACT CAG TTT GGT TTT TTG ATG GAA GTT 1846

S S A V F F F T D C L G E K E W D L L M 569
TCT TCA GCT GTG TTT TTT TTC ACT GAC TGT TTA GGT GAG AAG GAA TGG GAC TTG CTA ATG 1906

F L G E A A I E R C Y F V L S S Q A R E 589
TTT TTA GGA GAG GCT GCC ATT GAA AGA TGC TAC TTT GTT CTC AGT TCC CAA GCC AGG GAG 1966

S E E A Q I F Q R I L N L K P A Q L L F 609
AGT GAA GAG GCT CAA ATT TTT CAG AGG ATA CTG AAC TTG AAG CCA GCA CAG CTA CTG TTT 2026

W E R G D A G D R R K N M E G L Q A A L 629
TGG GAG AGG GGA GAT GCT GGG GAT AGA AGG AAG AAC ATG GAG GGC CTT CAA GCT GCC CTC 2086

Q E V M F S S C L R C V S V E D M A A L 649
CAG GAA GTG ATG TTC TCT TCT TGC CTC AGA TGT GTG TCT GTG GAG GAT ATG GCC GCC CTG 2146

A R E L G I Q V D E D F E N T Q R I Q V 669
GCC AGG GAG CTG GGG ATT CAG GTA GAT GAA GAC TTT GAA AAC ACT CAG AGA ATT CAA GTT 2206

S S G E N M A G T A E G E G Q Q R H S Q 689
TCC TCT GGA GAA AAC ATG GCT GGG ACA GCT GAA GGT GAG GGT CAG CAA AGA CAC AGT CAG 2266

L K S S S K S Q A L M P I Q E P G T Q C 709
CTA AAA AGC TCA TCT AAA AGC CAG GCT CTA ATG CCA ATT CAA GAG CCT GGG ACT CAA TGT 2326

E L S Q N L Q N L Y G T P V F R P V L E 729
GAG CTC AGC CAG AAT CTT CAG AAT CTC TAT GGT ACC CCA GTA TTC AGG CCT GTT CTA GAG 2386

N S W L F P T R I G G N F N H V S L K A 749
AAC TCC TGG CTC TTT CCA ACC AGA ATT GGA GGT AAC TTT AAC CAT GTT TCC TTG AAA GCC 2446

S W V M G R P F G S E Q R P K W F H P L 769
TCC TGG GTT ATG GGC CGC CCC TTT GGG TCA GAG CAG AGG CCT AAG TGG TTC CAT CCT TTG 2506

FIG. 28B



P F Q N A G A Q G R G K S F G I Q S F H 789
CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAAGACTACTGTCTATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTGTTT 3471

TTTGAGACAGAGTTTCACTCTTGTTGCCAGGCTGGAGTGCAATGGCAGCATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTT 3629

TATTTTATAGTAGAGGCAGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCCACCTA 3708

GGCCTCTCAAAGTGTGGGATTACGTGTGTAAGCCACAGTGCCCGAGCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATGAAAATAATTAAGACTAGAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGACCCAGGGAATGGGGTCTATGAGACAACCCCACTTGGAGAAGAATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTGACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

FIG. 28C



GCTCCAGAGGTATCTTTGTCAAAAGCTTCTGTTCAATATCAGCCACTGAGCAGATAACCCCTGCTTATTGGTGGTT 4103
AAATCAACTAGCTTCTGCTAATAGCCCCCAATTGCTTGAATGGGAAAACTCTCTCATTGGACCCCTTATAGGTAGAAATA 4182
ATGAATTAAACAACCAATAAAATTAATCAATTGGCAATTAATAAAAAAAAAAAAAAAAAAAAAA 4244

FIG. 28D

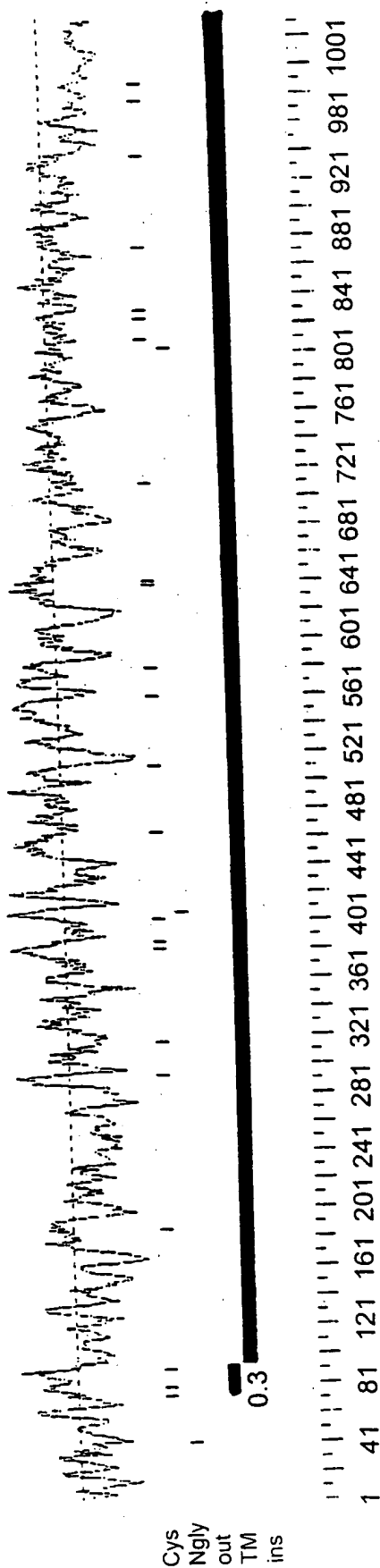


FIG. 29



NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

```
CONSENSUS      *-->maederrllkknrvrliesLgldvLdelldvLlekdvlnlkeeEkik
                +++ + ++ r++l+e+L+ d +Ld L +++++ ++e E
CARD6          5  STP--SEIIERERKKLLEILQHD-PDSILDTLTSRRLLISEEEYETLE 48

CONSENSUS      ragakledDKarelvdsIqrrgsqafdaIdaledTgqsyLAdvLel<--*
                + l + r l++ +q++g. + ++ f+ +l++ LA++ +l
CARD6          49 NVTDLLKK--SRKLLILVQKKGEATCQHFLKCLFS-TFPQLAAICGL 92
```

FIG. 30

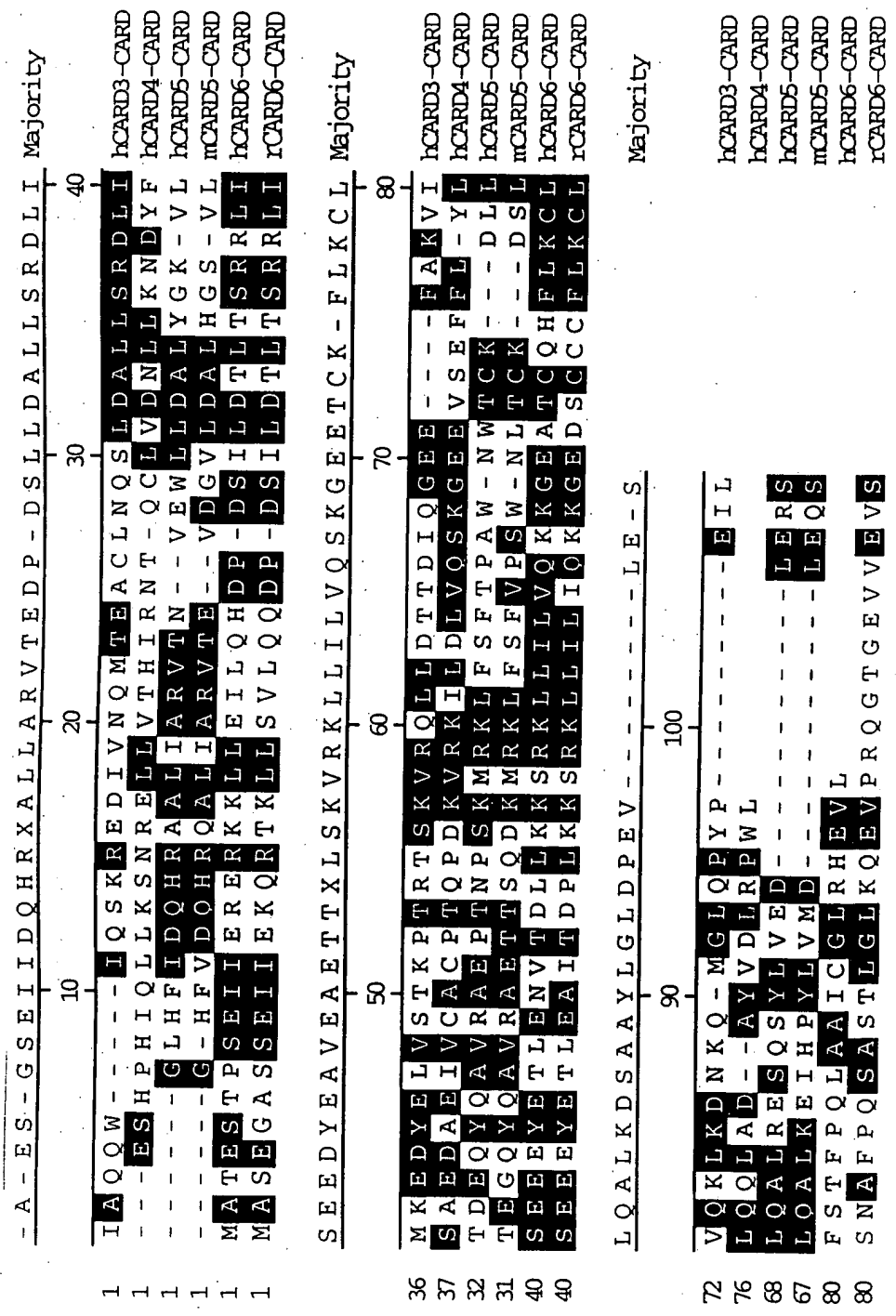


FIG. 31